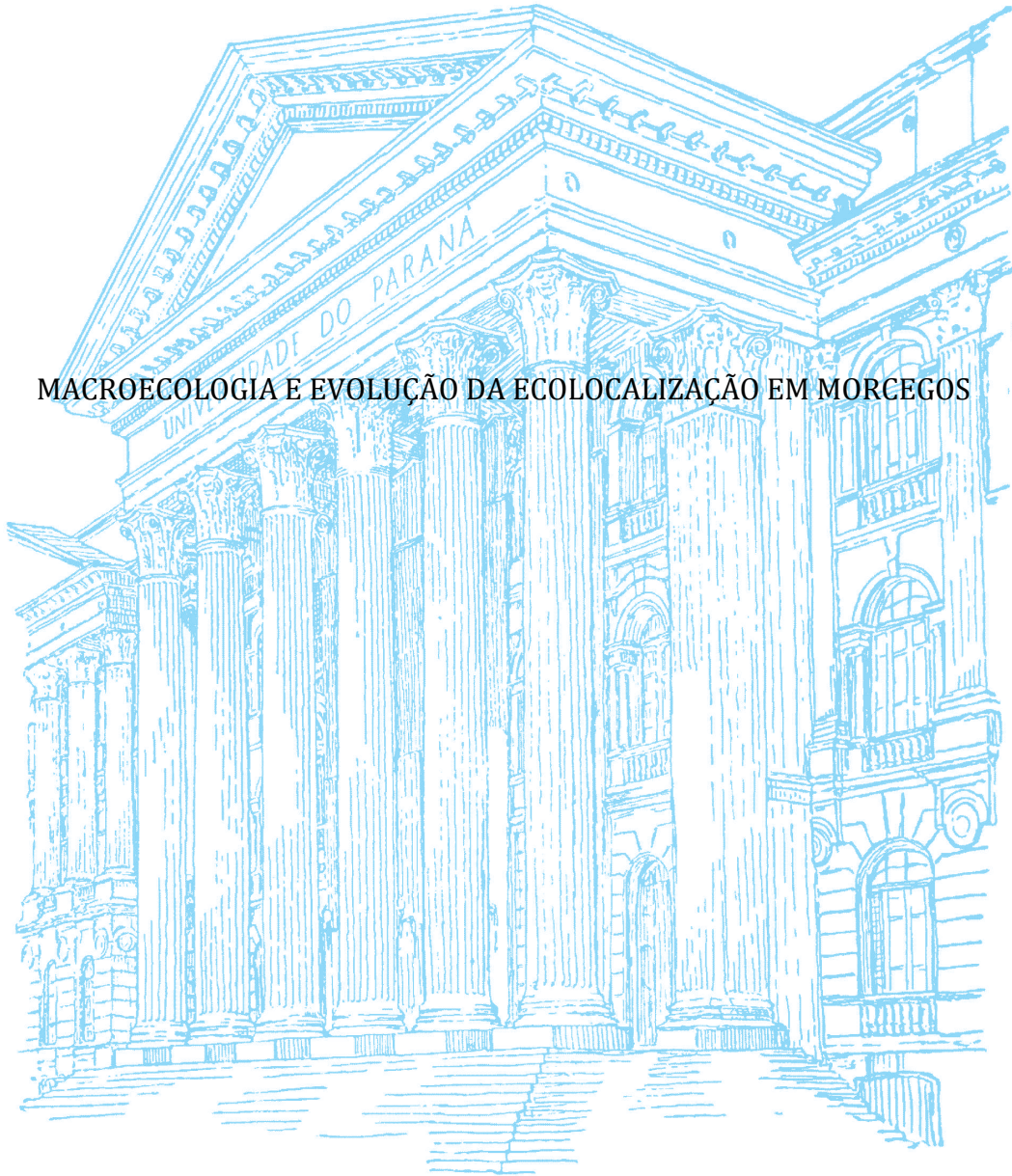


UNIVERSIDADE FEDERAL DO PARANÁ  
PROGRAMA DE PÓS-GRADUAÇÃO EM ECOLOGIA E CONSERVAÇÃO

DIEGO ROBERTO BILSKI

MACROECOLOGIA E EVOLUÇÃO DA ECOLOCALIZAÇÃO EM MORCEGOS



CURITIBA

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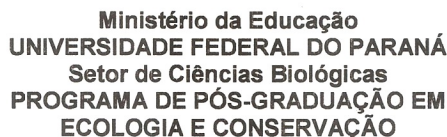
Tese apresentada ao Programa de Pós-Graduação em Ecologia e Conservação, Setor de Ciências Biológicas, Universidade Federal do Paraná, como requisito parcial à obtenção do título de Doutor em Ecologia.

Orientador: Prof. Dr. Marcio Roberto Pie

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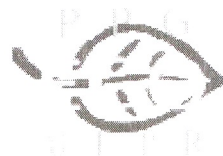
  
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## PARECER

Os abaixo-assinados, membros da banca examinadora da defesa da tese, a que se submeteu **Diego Roberto Bilski** para fins de adquirir o título de Doutor em Ecologia e Conservação, são de parecer favorável à **APROVAÇÃO** do trabalho de conclusão do candidato.

Secretaria do Programa de Pós-Graduação em Ecologia e Conservação.

Curitiba, 19 de março de 2015.

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## Agradecimentos

À toda minha família, por aturar meu mau humor nos últimos anos.

Ao meu orientador, por aturar minha esquisitice, longos períodos de silêncio e por me permitir trabalhar em casa.

Ao meu co-orientador, Brock Fenton, pelas discussões sobre morcegos, pós-graduação e ciência.

Também aos outros envolvidos no meu trabalho durante o período sanduíche, especialmente o Dr. Burton Lim, o colega Hao Li e a senhora responsável pela biblioteca, da qual não me recordo o nome. E também à doida que me hospedou durante esse período, Stoyanka Gerenska.

Aos amigos e colegas de laboratório, pós-graduação e vida acadêmica, especialmente à Viviane Deslandes, Gabriela Decker, Patrícia Ströher, Itiberê Bernardi, João Miranda, Andreas Meyer, Fernando Passos e Maurício Moura.

À CAPES pela concessão da bolsa e bolsa sanduíche.

Aos professores que aceitaram avaliar este manuscrito, Dr. Enrico Bernard, Dr. Fabrício Villalobos, Dr. Fernando de Camargo Passos, Dr. Maurício Osvaldo Moura e Dr<sup>a</sup>. Viviane Deslandes do Nascimento.

À Carina e à PB, por me lembrarem do que é importante.

## Resumo

Os morcegos constituem mais de 20% das espécies de mamíferos atualmente descritas, uma diversidade extraordinária ligada principalmente à capacidade de voo e à ecolocalização. A ecolocalização é um fenômeno presente em todas as famílias de morcegos. Das 19 famílias de morcegos atualmente reconhecidas, 18 emitem ecolocalização tonal produzida na laringe, enquanto espécies da família Pteropodidae emitem sons pulsados produzidos através de estalos da língua ou asas. Contudo, a ecolocalização em Pteropodidae é relatada para apenas algumas espécies, enquanto nas outras 18 famílias que emitem sons tonais esse sistema é ubíquo. A ecolocalização tonal é um sistema ativo relacionado principalmente com a localização espacial e navegação em ambientes escuros, mas também usada como método de detecção e classificação de itens alimentares em diversas espécies de morcegos. Diversos estudos oferecem hipóteses sobre a origem da ecolocalização, bem como hipóteses sobre a diferenciação dos chamados de ecolocalização em relação ao ambiente ocupado pelas diversas espécies de morcegos e a convergência dos tipos de chamados entre grupos filogeneticamente distantes. No entanto, pouco se sabe sobre a dinâmica de evolução da ecolocalização tonal, as influências morfológicas e ambientais sobre a diferenciação desta característica, e a ligação entre o fenômeno da ecolocalização e a excepcional riqueza de espécies de morcegos. O objetivo deste trabalho é apresentar respostas a estas questões a partir de uma perspectiva macroevolutiva e macroecológica, oferecendo uma visão geral sobre as forças intrínsecas e extrínsecas que afetam a evolução desta característica e possibilitam a diversidade de espécies e sinais de ecolocalização observados atualmente.

A questão das características morfológicas e ambientais atuantes sobre a diversidade de sinais de ecolocalização é abordada com o uso de ferramentas de biologia comparativa, determinando os sinais filogenético e espacial presentes nos diferentes parâmetros espectrais e temporais da ecolocalização e definindo a direção e magnitude das influências morfológicas e ambientais sobre cada parâmetro. O componente de história filogenética é preponderante sobre a maior parte dos parâmetros analisados, porém apenas a duração do chamado de ecolocalização apresenta um componente espacial próximo de zero. A amplitude de frequências no chamado aparece como o parâmetro com maior componente espacial, superior ao filogenético, e também apresenta a maior proporção de variação independente tanto da filogenia quanto do espaço. A frequência inicial também apresenta-se como um parâmetro relativamente mais plástico, enquanto a frequência final e a duração do chamado mostram menor variação independente e maior proporção de sinal filogenético. O pico de frequência mostra um componente filogenético intermediário entre a frequência inicial e final, e um componente independente superior ao espacial. A razão de aspecto da asa e o tamanho corporal (representado pelo tamanho de antebraço) têm as maiores influências sobre os parâmetros analisados, confirmando que animais maiores emitem chamados de frequência mais baixa e de maior duração. A temperatura também apresenta influência sobre a maioria dos parâmetros de ecolocalização, levando a frequências

mais altas e de menor duração. Os resultados confirmam algumas relações alométricas propostas em outros estudos, porém aqui controlando a autocorrelação filogenética entre as espécies, e demonstram heterogeneidade nos fatores filogenéticos e espaciais atuantes sobre o biosonar.

A relação entre os parâmetros de frequência e a duração dos chamados de ecolocalização leva à formação de algumas configurações espectro-temporais distintas, ligadas principalmente ao tipo de ambiente onde as espécies forrageiam mas também aos clados a que pertencem. Essas conformações muitas vezes são convergentes entre grupos distantes de morcegos que se utilizam de estratégias de forrageamento e/ou ocupam ambientes similares, porém não se sabe como esses casos de convergência se refletem na dinâmica de evolução das frequências de ecolocalização e sua relação alométrica com o tamanho de corpo. Avaliou-se então se essas diferentes conformações levam a diferentes taxas de evolução da frequência de máxima energia e do tamanho de antebraço, sob 18 hipóteses de cenários evolutivos que variam de uma taxa única para todos os clados até seis diferentes taxas evolutivas e convergências entre clados. A hipótese que melhor explica a variação encontrada na ecolocalização das espécies atuais de morcegos aponta quatro diferentes taxas de evolução, e apenas um caso claro de convergência nessas taxas. A grande maioria das espécies conserva a mesma taxa evolutiva encontrada no tipo de chamado apontado como ancestral aos morcegos que emitem ecolocalização tonal, enquanto alguns clados que emitem chamados de baixa amplitude de frequências apresentam taxas mais baixas ou mais elevadas em relação ao estado ancestral. O mesmo cenário explica também a variação no tamanho de antebraço, porém as taxas de diferenciação são menores do que aquelas da ecolocalização. Os resultados demonstram que apesar das convergências na relação espectro-temporal entre alguns grupos, as taxas de evolução da ecolocalização e tamanho de antebraço comumente seguem o padrão encontrado nos clados a que os grupos pertencem. A relação alométrica entre ecolocalização e tamanho corporal também se reflete nas diferenças de taxas evolutivas entre clados, porém em velocidades diferentes.

Sabe-se que a ordem Chiroptera apresenta uma forte relação entre a riqueza de espécies e a temperatura, formando um pronunciado gradiente latitudinal de riqueza ligado à conservação filogenética do nicho climático tropical. Porém os mecanismos ligando a coexistência de várias espécies em escala local com os padrões regionais de riqueza são desconhecidos. A atenuação acústica gerada pela atmosfera, uma função não linear da temperatura, umidade e frequência sonora, pode atuar como um mecanismo de facilitação da coexistência diminuindo a interferência acústica entre hetero- e coespecíficos. Essa hipótese é testada primeiramente buscando-se a melhor combinação de variáveis ambientais que explicam o gradiente de riqueza de espécies que ecolocalizam, e avaliando a capacidade desse modelo em prever a riqueza de espécies que não possuem ecolocalização tonal. Em seguida, avaliou-se o papel da atenuação sonora diretamente sobre o padrão de riqueza de espécies através de modelos generalizados aditivos. A combinação entre temperatura e umidade, variáveis responsáveis pela atenuação sonora, é a que melhor explica o gradiente de riqueza das espécies que ecolocalizam, porém este modelo prediz uma riqueza de espécies



muito maior do que a observada para as espécies que não ecolocalizam. A atenuação sonora explicitamente modelada responde por 79% da variação no gradiente de riqueza de espécies, excedendo a variação explicada simplesmente pela temperatura e umidade em separado. Esses resultados fornecem evidências de que a atenuação sonora pode ser o principal mecanismo de ligação entre os processos locais e regionais que determinam o gradiente de riqueza de espécies de morcegos que emitem ecolocalização tonal.

## Abstract

Bats constitute more than 20% of the currently known mammal species, an exceptional diversity linked to powered flight and echolocation. Eighteen from the 19 bat families use tonal echolocation produced in the larynx, while species from the Pteropodidae family use tongue or wing clicks in some circumstances. However, only a few species of Pteropodidae are known to produce echolocation, while tonal echolocation is ubiquitous in all species from the other 18 families. Tonal echolocation is an active system commonly used for spatial navigation in low-light conditions, but a large number of species also use it to detect and classify food items. Several studies offer hypotheses about the origin of echolocation and the differentiation between echolocation types in relation to habitat, as well as the convergence of echolocation designs among phylogenetically distant groups. However, the dynamics of the tonal echolocation evolution, the influences of morphological and environmental variables, and the mechanisms linking echolocation to the exceptional bat diversity are poorly known. This work presents answers to these questions from a macroevolutionary and macroecological perspective, offering a broad-scale assessment of the intrinsic and extrinsic forces that shape this characteristic and allow the observed diversity of species and echolocation signals.

Comparative biology tools are used to determine the morphological and environmental variables shaping the diversity of echolocation calls, establishing the phylogenetic and spatial signals in the different spectral and temporal parameters of echolocation, and analyzing the direction and magnitude of the morphological and environmental influences. The phylogenetic component is preponderant in almost all parameters analyzed, although only the call duration shows a nearly absent spatial component. Call bandwidth appears as the most spatially structured parameter, greater than the phylogenetic signal, and also has the greatest variation independent from both phylogeny and space. The initial frequency also appears as a relatively plastic characteristic, while the final frequency and call duration show the smallest independent component and a greater contribution of phylogenetic history. The peak frequency has a phylogenetic component in between that of the initial and final frequencies, and an independent component greater than the spatial one. Wing's aspect ratio and body size (represented by the forearm length) have the greatest influence over the analyzed parameters, confirming the proposition that larger species emit calls of lower frequencies and longer durations. Temperature is also influential over most of the analyzed parameters, leading to higher frequencies and lower durations in the warmest regions. The results corroborate some of the proposed allometric relationships between echolocation and body size, but here controlling for the phylogenetic autocorrelation among species, and demonstrate the heterogeneity in the phylogenetic and spatial influences over the biosonar variation.

The relationship between frequency parameters and call duration leads to some distinct spectrotemporal configurations, majorly linked to the habitat in which the species forage, but also to their phylogenetic positions. These call designs are

often convergent between distantly related groups that forage and/or occupy similar habitats, however little is known about how these cases of design convergences translate into the dynamics of evolution of echolocation frequencies and their allometric relationship with body size. This work evaluates whether these different call designs lead to different rates of frequency of maximum energy and forearm length evolution, evaluating 18 hypothetical scenarios that vary from a single rate of evolution for all bat species to a scenario of six different rates and cases of convergences between clades. The hypothesis that better explains the variation in echolocation frequencies among current bats is composed by four different rates of phenotypic differentiation and just one clear case of convergence in these rates. The vast majority of species retains the same rate of the echolocation type found to be the ancestral state of laryngeal echolocating bats, while some clades that emit narrowband calls have rates lower or higher than the ancestral background. The same scenario explains the variation in forearm length, yet with rates always lower than those found for echolocation frequency. The results show that, despite the convergences in call shape between some groups, rates of frequency and body size evolution often follow the pattern of the clades to which the groups pertain. The allometric relationship between echolocation and body size is also reflected in the rates of phenotypic differentiation, although with disparate paces.

It is known that Chiroptera shows a strong relationship between species richness and temperature, leading to a pronounced latitudinal richness gradient linked to the phylogenetic conservatism of the tropical niche. However, the mechanisms linking the coexistence of species in local scale with the regional patterns are poorly known. Atmospheric sound attenuation, a nonlinear function of temperature, humidity and sound frequency, can act as a mechanism that facilitates the coexistence through diminishing the acoustic interference between hetero- and conspecifics. This hypothesis is tested through assessing the environmental predictors that best explain the richness gradient of echolocating bats, and then evaluating the capacity of this model in predicting the richness gradient of non-echolocating species. Further, the role of atmospheric sound attenuation in shaping the echolocating species richness is directly evaluated through generalized additive models. As expected, the model composed by temperature and humidity, the variables responsible for sound attenuation, has the best fit to the richness gradient of echolocating bats, but this model greatly overpredicts the richness of non-echolocating bats. The explicitly modeled atmospheric sound attenuation accounts for 79% of the variation in the richness gradient, exceeding the variation explained by a model composed by temperature and humidity separately. These results show that sound attenuation can be the principal mechanism linking the local and regional scale processes that shape the richness gradient of laryngeal echolocating bats.



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## Introdução geral

Com cerca de 1100 espécies atualmente descritas, os morcegos representam mais de 20% das espécies de mamíferos atuais (Simmons 2005a). Exceto pela ausência na Antártica, estes animais são abundantes e diversos em todos os continentes, apresentando um amplo espectro de recursos alimentares utilizados, como insetos, frutos, néctar, pequenos vertebrados, peixes e sangue (Simmons & Conway 2003). A capacidade de voo verdadeiro e a ecolocalização são tidas como as maiores responsáveis por essa grande riqueza de espécies de morcegos e pela sua capacidade em explorar diversos nichos (Jones & Teeling 2006, Simmons 2005b).

O parco registro fóssilífero de morcegos aponta para uma grande explosão adaptativa durante o Eoceno, quando teriam surgido todas as linhagens atualmente existentes (Simmons 2005b). Nessa época geológica grande parte do globo apresentava climas semelhantes ao clima tropical atual, e a distribuição dos táxons atuais de morcegos sugere a conservação deste nicho climático (Buckley *et al.* 2010). Porém essa grande radiação adaptativa em um tempo relativamente curto dificulta a proposição de filogenias baseadas exclusivamente em caracteres morfológicos (Simmons 2005b, Teeling *et al.* 2005). Com isso, as adaptações para a ecolocalização foram e continuam sendo utilizadas como caracteres determinantes para a classificação das espécies (Arita & Fenton 1997, Simmons 2005a).

Como a ecolocalização é um sistema complexo que envolve especializações nos sistemas respiratório e nervoso central, além de adaptações morfológicas nas orelhas dos morcegos (Arita & Fenton 1997, Neuweiler 2003, Vater & Kössl 2004), assumiu-se, por vários anos, que esta adaptação teria surgido uma única vez durante a evolução do grupo (Simmons 2005b). Neste cenário, um único evento seria responsável pela divisão de um grupo capaz de ecolocalizar através da laringe (Microchiroptera) e outro sem esta capacidade (Megachiroptera), composto atualmente apenas pela família Pteropodidae (Kunz & Pierson 1994; Simmons 2005b). Contudo, um gênero desta família, *Rousettus*, possui espécies capazes de

ecolocalizar através de estalos produzidos pela língua (Holland *et al.* 2004, Yovel *et al.* 2010), enquanto membros de outras subfamílias de Pteropodidae ecolocalizam através de estalos produzidos com as asas (Boonman *et al.* 2014).

No entanto, contrariando o cenário evolutivo baseado em caracteres morfológicos e de ecolocalização, abordagens baseadas em caracteres moleculares postulam a separação dos morcegos capazes de ecolocalização em duas subordens: Yangochiroptera, composta por 13 famílias, e Yinpterochiroptera, com 6 famílias (Eick *et al.* 2005; Teeling *et al.* 2005). Neste último grupo está inclusa a família Pteropodidae, antes considerada como um grupo à parte na evolução de Chiroptera (Teeling *et al.* 2000). Neste cenário mais recente, consideram-se duas possibilidades para a evolução da ecolocalização: uma origem única, com posterior perda da capacidade de ecolocalização nos Pteropodidae, e ressurgimento secundário no gênero *Rousettus* (Teeling *et al.* 2000; Simmons 2005b); ou então a existência de dois eventos de evolução da ecolocalização, uma vez no ancestral de Yangochiroptera, e outra em Yinpterochiroptera, no ancestral comum do clado que exclui os Pteropodidae (Eick *et al.* 2005). Porém este evento evolutivo ainda é motivador de diversas discussões (Jones & Holderied 2007), e a recente descoberta da ecolocalização através de estalos das asas em outras subfamílias de Pteropodidae (Boonman *et al.* 2014) deve reacender esse debate (Fenton & Ratcliffe 2014).

Essa ecolocalização em espécies de Pteropodidae, no entanto, é produzida apenas em contextos específicos como modo de localização espacial, e difere estruturalmente da ecolocalização tonal, produzida na laringe, presente nas outras 18 famílias de morcegos (Schnitzler *et al.* 2003). A ecolocalização tonal pode servir a diversos propósitos, sendo a percepção do meio físico o mais óbvio deles (Fenton 1992, Simmons & Geisler 1998), provavelmente presente em todas as espécies capazes de ecolocalizar (Jones 1999). Já a detecção e localização de presas é algo que requer maior precisão e detalhamento do que o necessário para auxiliar na movimentação e detecção de grandes obstáculos (Fenton 1992), mas acredita-se que todas as espécies utilizam a ecolocalização em algum momento da obtenção do alimento (Kunz & Pierson 1994).

Essa gama de possibilidades de uso do biosonar é refletida no amplo



espectro de frequências capazes de serem emitidas pelas espécies de morcegos, que podem estender-se de 11 kHz a mais de 200 kHz (Jones 1999). A frequência dominante (Figura 1) emitida por uma determinada espécie comumente reflete o tipo de utilização que a espécie faz do biosonar (Simmons & Conway 2003). Por exemplo, a maior parte dos morcegos insetívoros que localizam suas presas através da ecolocalização emite frequências dominantes no intervalo entre 20 kHz e 60 kHz, o intervalo de frequência ideal para localizar pequenos insetos (Jones & Holderied 2007).

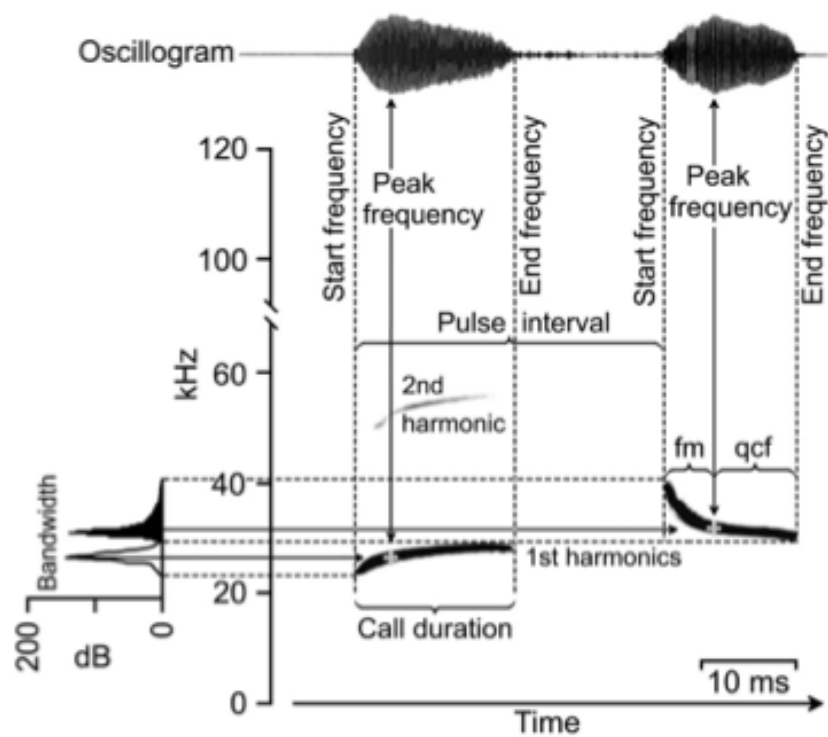


Figura 1: Parâmetros que compõem a ecolocalização, estimados a partir do espectrograma e oscilograma dos chamados em fase de busca. Extraído de Jung *et al.* 2014. Neste estudo são avaliados os parâmetros de frequência inicial, frequência final, pico de frequência, amplitude e duração.

Há diversos tipos de estratégias de ecolocalização encontrados em morcegos (Figura 2). Basicamente, estas estratégias podem ser categorizadas em três grupos, em relação à frequência e tempo de duração dos pulsos: (1) sinais de espectro amplo, que englobam uma grande quantidade de frequências e normalmente

emitidos por um curto período de tempo ( $<5\text{ms}$ ); (2) sinais de espectro reduzido, que distribuem-se por uma pequena faixa de frequências e comumente são mantidos por um longo período; e (3) sinais de frequência constante, mantidos por longos períodos de tempo ( $\pm 60\text{ms}$ ) em uma única frequência, permitindo a "classificação" do eco recebido pelos morcegos (Jones 2005). Esses tipos de sinais têm relação direta com o tipo de habitat onde as espécies forrageiam e/ou se deslocam (Figura 3; Schnitzler & Kalko 2001, Schnitzler *et al.* 2003). O intervalo entre os pulsos de ecolocalização, e em alguns casos também a estrutura, diferem de acordo com fases de detecção. A fase de busca caracteriza-se por intervalos mais longos, que gradualmente diminuem quando da aproximação em relação ao alimento até a formação de fases terminais (*terminal buzzes*), próximo da captura ou coleta do alimento (Griffin *et al.* 1960).

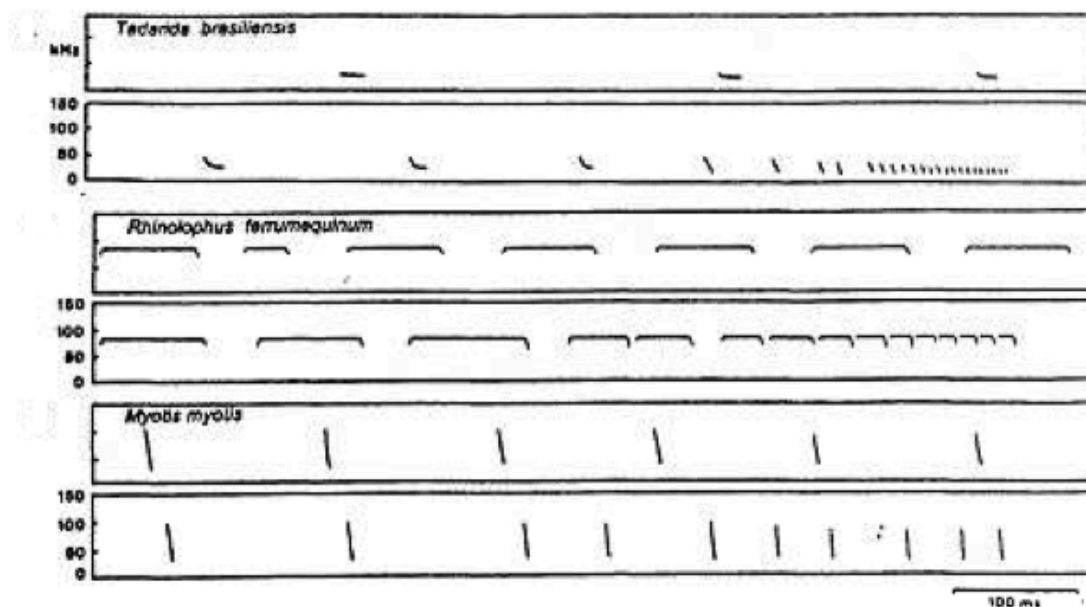


Figura 2: Padrões espectro-temporais (kHz x ms) em fase de busca (acima) e em fase terminal (abaixo) em três espécies de morcegos insetívoros. Em fase de busca, podem ser observados, respectivamente, exemplos de sinais de espectro reduzido (*Tadarida brasiliensis*), frequência constante (*Rhinolophus ferrumequinum*) e espectro amplo (*Myotis myotis*). Modificado de Schnitzler & Kalko 2001.

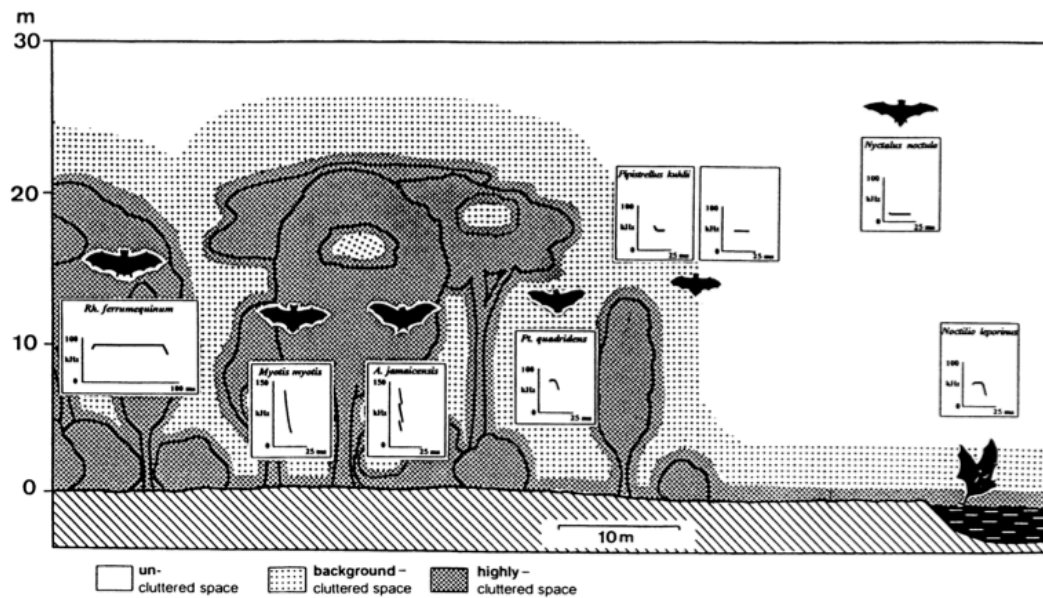


Figura 3: Esquema simplificado da relação entre os padrões espectro-temporais de ecolocalização e o tipo de habitat utilizado pelas espécies. Os habitats dividem-se de acordo com a densidade da vegetação, caracterizando ambientes totalmente abertos, onde prevalecem ecolocalizações de baixa frequência e espectro reduzido; ambientes próximos à borda da vegetação e próximos ao solo e corpos d'água, onde predominam sinais de espectro reduzido e frequências altas; e ambientes de dominados por vegetação, onde sinais de espectro amplo e frequência constante são mais comuns. Extraído de Schnitzler & Kalko 2001.

A ecolocalização é um processo energeticamente dispendioso, com o custo energético para a emissão de pulsos de ecolocalização equiparável ao custo energético do voo nestes animais (Speakman *et al.* 1989). Porém, de acordo com experimentos realizados com algumas espécies, acredita-se que a maioria dos morcegos sincroniza a emissão de pulsos com o movimento das asas, o que praticamente anula o custo energético da emissão dos pulsos, pois os mesmos grupos musculares são utilizados nos dois processos (Rayner 1991; Speakman & Racey 1991, Voigt & Lewontin 2012). Com vistas à economia de energia, portanto, a taxa ótima de emissão de pulsos seria regulada pelo tamanho dos animais, ou talvez mais especificamente pelo tamanho de suas asas (Jones 1999, Holderied & von Helversen 2003). Além disso, a frequência da ecolocalização apresenta também uma



relação negativa com o tamanho da espécie, por conta das cordas vocais mais longas em animais maiores (Jones 1999).

Além do tamanho dos animais e dos custos energéticos, fatores ambientais e as propriedades físicas do som exercem também pressão seletiva sobre a ecolocalização em morcegos (Lawrence & Simmons 1982, Snell-Rood 2012). Frequências mais baixas, apesar de menos dispendiosas energeticamente, são incapazes de prover detalhes precisos e, portanto, seriam de pouca utilidade para espécies que capturam insetos em voo (Jones 1999, Fenton *et al.* 1998). Por outro lado, frequências mais altas são atenuadas pelo ar e pela umidade mais rapidamente, o que diminui a distância de alcance da ecolocalização (Fenton 1992, Stilz & Schnitzler 2012). Com isso, morcegos enfrentam um *trade-off* entre detalhamento e alcance de seu biosonar.

Comunidades de morcegos nas regiões tropicais podem conter mais de 50 espécies (e.g. Kingston *et al.* 2000), o que leva a questões sobre os mecanismos de coexistência, pois há a necessidade individual de reconhecimento do próprio pulso de ecolocalização (Obrist 1995, Barclay 1999). Além disso, sabe-se que a ecolocalização é também utilizada na determinação de espaçamento inter-individual durante o forrageio (Altringham & Fenton 2003), e a partilha do nicho acústico entre as espécies é reconhecida em diversas comunidades (e.g. Heller & von Helversen 1989, Kingston *et al.* 2000, Russo *et al.* 2007). Diferenças nos padrões de ecolocalização capacitam as espécies a forragearem a diferentes distâncias da vegetação (Siemers & Schnitzler 2004, Schmieder *et al.* 2012), mas não necessariamente revelam diferenças na utilização de recursos alimentares. Ao contrário, podem estar apenas refletindo a necessidade de reconhecimento da ecolocalização por parte da espécie (Kingston *et al.* 2001). Mais que isso, esses padrões podem também apontar a existência de diferenças entre espécies morfológicamente similares (Jones & Pardijs 1993; Kingston *et al.* 2001).

Apesar de ser reconhecido que a ecolocalização apresenta padrões espécie-específicos (Simmons & Conway 2003; Teeling *et al.* 2000), até o momento as perspectivas filogenéticas existentes sobre este processo são baseadas principalmente em revisões não sistematizadas, e o abordaram ou através de

padrões muito generalizados, que consideram apenas características comuns dentro das famílias de Chiroptera (e.g. Eick *et al.* 2005, Jones & Teeling 2006), ou então em estudos de comunidades pontuais (e.g. Kingston *et al.* 2000), que não refletem satisfatoriamente a filogenia dos grupos. Do mesmo modo, as relações alométricas da ecolocalização com a morfologia são descritas sem levar em conta as relações filogenéticas entre as espécies (e.g. Aldridge & Rautenbach 1987, Norberg & Rayner 1987, Jones 1999), o que compromete o poder estatístico das análises utilizadas nestes estudos (Harvey & Pagel 1991, Diniz-Filho 2000).

Caracteres fenotípicos comuns às espécie de um clado geralmente remontam a uma origem única, e as variações interespecíficas nesses caracteres muitas vezes são proporcionais ao tempo de divergência entre as linhagens (Felsenstein 1985). Dessa forma, as espécies não constituem amostras independentes para fins estatísticos, e análises que levam em conta esta autocorrelação filogenética devem ser usadas em estudos comparativos (Felsenstein 1985, Harvey & Pagel 1991). Pares de espécies filogeneticamente mais próximos, portanto, geralmente são mais similares entre si do que com espécies filogeneticamente mais distantes (Blomberg *et al.* 2003), um padrão definido como sinal filogenético (revisado em Munkemüller *et al.* 2012). As métricas mais utilizadas para quantificar o sinal filogenético avaliam o grau em que a variação interespecífica pode ser predita pelo tempo de divergência entre as linhagens (Pagel 1999, Freckleton *et al.* 2002, Blomberg *et al.* 2003, Munkemüller *et al.* 2012). Do mesmo modo, se um dado caráter evolui em resposta a variáveis ambientais, espécies que ocupam regiões geograficamente próximas podem ser mais similares entre si do que com espécies que ocupam regiões mais distantes (Lennon 2000, Freckleton & Jetz 2009), e uma medida da autocorrelação espacial deve ser levada em conta para controlar os efeitos da variação que se devem à proximidade geográfica entre as espécies (Diniz-Filho *et al.* 2007, Freckleton & Jetz 2009).

Portanto, a investigação sobre as variáveis que influenciam na evolução de um caráter, bem como dos processos evolutivos responsáveis pelas diferenças entre espécies e clados, requer a inclusão do conhecimento sobre as relações filogenéticas entre as espécies. No entanto, até o momento poucos estudos sobre a evolução de

morcegos se utilizaram da informação filogenética de forma direta (e.g. Davies *et al.* 2013, Jacobs *et al.* 2014), e estudos sobre a evolução da ecolocalização para a ordem Chiroptera como um todo ainda são inexistentes. Dessa forma, o presente estudo visa integrar a informação filogenética para quantificar os sinais filogenético e espacial nos diferentes parâmetros da ecolocalização (Figura 1), bem como avaliar as influências morfológicas e ambientais sobre a variação fenotípica nesses parâmetros; analisar a dinâmica de evolução do pico de frequência e sua relação com o tamanho de corpo; e investigar a ligação entre a ecolocalização e os padrões globais de diversidade de espécies de morcegos.

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## **CAPÍTULO 1**

### **HISTORICAL AND SPATIAL STRUCTURES IN BAT ECHOLOCATION**

## 1.1 Introduction

Bats constitute more than 20% of mammalian species (Simmons 2005a), an exceptional diversity assumed to be linked to the evolution of powered flight and echolocation (Simmons 2005b, Teeling *et al.* 2005, Jones & Teeling 2006). Almost 85% of all bat species emit tonal echolocation signals produced in the larynx (Schuller & Moss 2004), while some species in Pteropodidae, the one family that do not produce laryngeal echolocation, use tongue or wing clicks to navigate in darkness (Gould 1988, Yovel *et al.* 2010, Boonman *et al.* 2014). Most laryngeal echolocators use it to navigate and recognize ambient features at low or absent light (Griffin 1946, Moss & Surlykke 2010, Boonman *et al.* 2013), but many species also use echolocation to find and track prey items (Griffin *et al.* 1960, Korine & Kalko 2005). Echolocation calls often have species-specific components (O'Farrell *et al.* 1999, Russo & Jones 2002, Schnitzler *et al.* 2003), generating a diversity of echolocation signals linked to foraging habitat (Schnitzler & Kalko 2001, Schnitzler *et al.* 2003), food acquisition (Denzinger & Schnitzler 2013) and phylogenetic history (Jones & Teeling 2006). However, despite the recognition that phylogenetic relationships are responsible for part of the echolocation similarities among species (Jones & Holderied 2007, Jones & Siemers 2010), a formal quantification of the amount of phylogenetic signal (Blomberg *et al.* 2003, Münkemüller *et al.* 2012) is lacking.

Phylogenetic signal can be defined as the tendency of closely related species to resemble each other more than they resemble species drawn at random from the tree (Blomberg & Garland 2002). This phenomenon can result simply from the hierarchical structure of the tree, and do not require evolutionary processes like adaptation and natural selection (Hansen & Martins 1996, Blomberg & Garland 2002). Several metrics to quantify this phylogenetic dependency among species have been proposed (reviewed and evaluated in Nunn 2011, Münkemüller *et al.* 2012), among which two stand out by providing indices that can be directly compared among phylogenies: Pagel's  $\lambda$  (Pagel 1999, Freckleton *et al.* 2002) and Blomberg's K (Blomberg *et al.* 2003). Both indices are based on a Brownian motion



model of character evolution, where the variance in trait values is proportional to the time of divergence among taxa (Felsenstein 1985). Because of this phylogenetic dependency, statistical analyses of interspecific data must take into account the phylogenetic relatedness among species to circumvent the non-independence in species observations (Felsenstein 1985, Harvey & Pagel 1991, Revell 2010). Likewise, species that share a common habitat can show more similarities than a random pair of species, due to their similar environment (Lennon 2000, Diniz-Filho *et al.* 2007), and thus a quantification of both phylogenetic and spatial signals can help to understand the processes that shape phenotypic diversity through disentangling these sources of autocorrelation (Freckleton & Jetz 2009; Cooper *et al.* 2011).

To effectively probe the environment and localize food through the biosonar, bats need to integrate several sources of echoes to form a detailed image of the surroundings and the focused food item (Moss & Surlykke 2010). This is achieved through adaptations in the timing, frequency, intensity, duration, and sonar beam shape (Surlykke *et al.* 2009, Moss & Surlykke 2010, Jakobsen *et al.* 2012). The foraging habitat and functional guild are regarded to have prominent roles in determining the structural relationship between frequency and time within calls (Schnitzler & Kalko 2001, Surlykke & Kalko 2008, Denzinger & Schnitzler 2013), leading to cases of convergent call designs among distantly related groups (Jones & Teeling 2006). Despite these habitat-associated similarities, species often differ in some components in species-specific manners (Fenton & Bell 1981, O'Farrel *et al.* 1999, Russo & Jones 2002, Schnitzler *et al.* 2003, Walters *et al.* 2012). Several mechanisms of frequency segregation among sympatric and/or sister species have been proposed, including differences in body size (Heller & von Helversen 1989, Jones 1999), prey size preferences (Jones & van Parijs 1993, Houston *et al.* 2004, Safi & Siemers 2010), and intraspecific communication (Heller & von Helversen 1989, Thabab *et al.* 2006, Russo *et al.* 2007, Jones 2008, Jones & Siemers 2010).

Several studies disregard the trophic niche partitioning as a driver of echolocation frequency divergence, arguing that the differences in detection resolution between similar frequencies are negligible, and finding significant dietary

overlap (e.g. Kingston *et al.* 2001, Jones & Barlow 2004, Thabah *et al.* 2006, Jacobs *et al.* 2007, Russo *et al.* 2007, Jones & Siemers 2010). As well, intraspecific communication (see Jones 2008, Jones & Siemers 2010) not necessarily holds as the principal mechanism driving the maintenance of species-specific frequencies, given that the major purpose of echolocation – self-recognition of the emitted call (Obrist 1995, Barclay 1999) – is also facilitated by these call differences. Moreover, several species have social call repertoires different from the echolocation calls used for searching prey (e.g. Barclay *et al.* 1979, Barlow & Jones 1997, Pfalzer & Kusch 2003, Chaverri *et al.* 2010), and these social calls are more variable than echolocation ones (Fenton 1994). Bats may indeed be attracted by echolocating conspecifics, particularly those emitting feeding-buzzes (Gillam 2007, Cvikel *et al.* 2015a), but this attraction may elicit frequency alterations to avoid jamming (Ulanovsky *et al.* 2004, Gillam *et al.* 2007, Takahashi *et al.* 2014, but see Cvikel *et al.* 2015b), as well as antagonistic behaviors (Barlow & Jones 1997, Corcoran & Conner 2014).

The most consistent scaling of echolocation parameters is that with body size (Jones 1999). Both frequency (Aldridge & Rautenbach 1987, Norberg & Rayner 1987, Jakobsen *et al.* 2012) and time (Holderied & von Helversen 2003) parameters have a significant relationship with wing size and body mass, although there are known cases of deviations from this allometric scaling (Jacobs *et al.* 2007), as well as morphologically similar sister species with different echolocation frequencies (Jones & van Parijs 1993, Thabah *et al.* 2006). Nonetheless, this allometric scaling has been established without taking into account the phylogenetic relatedness among species (but see Jacobs *et al.* 2007, 2014), what can hamper its conclusions (Martins & Hansen 1997, Garland *et al.* 1999). Moreover, tonal calls comprise several spectral and temporal parameters, which serve different functions (Holderied & von Helversen 2003, Siemers & Schnitzler 2004), and thus may present disparate amounts of phylogenetic and spatial signals (McCracken & Sheldon 1997) as well as different relationships with morphological and environmental variables.

In this work we aim to investigate the magnitudes of the phylogenetic and spatial signals in the evolution of echolocation frequency and time parameters, and establish their relationships with morphological and environmental variables using

phylogenetically corrected regressions. Species often show similarities in structural and frequency parameters with those of its congeners (e.g. Taylor 1999, Russo & Jones 2002, see also Jones & Teeling 2006), so we can expect a relatively high amount of phylogenetic signal in some echolocation parameters. However, it is known that closely related species do differ in call bandwidth according to the habitats they forage in (Siemers & Schnitzler 2004), and whether the similarities in other call parameters among related species are due to habitat or phylogenetic structure is not thoroughly understood. We do not include the echolocating species from the family Pteropodidae because their echolocation is specialized and produced in a different way from laryngeal echolocation (Holland *et al.* 2004, Yovel *et al.* 2010, Boonman *et al.* 2014). We here intend to look into the macro-evolutionary and ecological grounds of tonal echolocation evolution, and hence we overlook the fine-scale alterations adopted by bats in specific situations (e.g. Brinkløv *et al.* 2010, Chiu *et al.* 2010, Bates *et al.* 2011, Falk *et al.* 2014) and the geographical intraspecific differences that are documented for some species (e.g. Guillen *et al.* 2000, Armstrong & Coles 2007, Chen *et al.* 2009, Veselka *et al.* 2013).

## 1.2 Material and Methods

### 1.2.1 Data collection:

We compiled echolocation parameters from published articles, theses, and field guides (see Table 1 for description of the studied parameters, and supplementary Table S1 for the references used for each species). Only calls explicitly measured during the search phase (Griffin *et al.* 1960) were used. The number of reported parameters varied considerably between sources, resulting in a final dataset with different levels of resolution for each parameter. Weighted averages were computed for each parameter, considering the sample size indicated in each source, and assuming a sample of just one individual when this information

was absent. We obtained wing measurement variables from 278 species at the Royal Ontario Museum mammal collection (29% of the echolocating bats based on Wilson & Reeder 2005. See Table S1 for a complete description of the dataset representativeness). Given that dried skins account for the majority of species in this collection, preventing the calculation of wing areas, we used two wing parameter indices proposed by Findley *et al.* (1972) (i.e. aspect ratio index and tip index; Table 2), as well as the forearm length. Additional forearm length information was obtained from the PanTHERIA dataset (Jones *et al.* 2009).

TABLE 1: Echolocation variables investigated in the present study. N corresponds to the available number of species for each parameter. See supplementary Table S2 for details on sample sizes and the parameters available for each species.

Parameter	Description	N
Peak frequency	The frequency with maximal amplitude (kHz)	262
Initial frequency	Starting pulse frequency (kHz)	240
Final frequency	Frequency at the end of the pulse (kHz)	243
Bandwidth	Difference between the initial and final frequencies (kHz)	251
Duration	Duration of the echolocation pulse (ms)	252

TABLE 2: Morphological and environmental variables used to model interspecific variation in echolocation acoustic parameters.

Parameter	Description
Forearm length	Length between the elbow and the wrist (mm)
Aspect ratio index	Length of (Digit III + Forearm) / Digit V
Tip index	Digit III / Forearm
NDVI	Normalized difference vegetation index
Bio01	Annual mean temperature
Bio04	Temperature seasonality
Bio28	Annual mean moisture index
Bio31	Moisture index seasonality

We combined geographical range maps obtained from the IUCN global mammal assessment (IUCN 2013) with four bioclimatic rasters from the CliMond

v1.1 dataset (Table 2; Kriticos *et al.* 2011) to estimate the average climatic conditions (environmental centroid) experienced by each species. Annual precipitation and precipitation seasonality were not included in further analyses due to their high correlation with mean annual moisture and moisture seasonality ( $r = 0.92$  for both pairwise comparisons). We selected temperature and moisture variables because they are involved in atmospheric sound attenuation (Stilz & Schnitzler 2012), and the mean annual NDVI (FAO 2008) was selected to represent forest cover. The data extraction was performed using the `raster` 2.2-12 package (Hijmans 2014), in R 3.0.2 (R Core Team 2013). Phylogenetic information on the studied species was based on the ‘best dates’ supertree by Fritz *et al.* (2009). This tree is only 51% resolved, so we used 100 possible polytomy resolutions provided by Kuhn *et al.* (2011), considering them as equivalent to a Bayesian posterior distribution of trees. Fritz *et al.* tree represents an updated version of the Bininda-Emonds *et al.* (2007, 2008) supertree, after correcting some of the species names. We visually checked the bat nomenclature in the obtained tree, and found 60 additional incorrect species names, based on the Wilson and Reeder (2005) classification, the same used by the IUCN global mammal assessment. These names were corrected before the analyses, and the same nomenclature corrections were applied to Kuhn’s *et al.* (2011) trees.

### 1.2.2 Analyses:

To determine the amount of phylogenetic and spatial autocorrelation in echolocation parameters, we used the method proposed by Freckleton & Jetz (2009) to estimate three parameters, namely  $\phi$ ,  $\lambda'$  and  $\gamma$ .  $\phi$  measures the relative contribution of spatial and phylogenetic effects, and varies between zero (no spatial effect) and one (all the variation explained by the geographical distance).  $\lambda'$  is the spatially corrected version of Pagel’s  $\lambda$  (Pagel 1999, hereafter  $\lambda_P$ ), and is estimated as  $(1 - \phi) \lambda_P$ . Its definition follows the one proposed by Pagel (1999), varying from

zero (phylogenetic independence) to one (where trait values are structured according to a Brownian motion model of evolution). Finally,  $\gamma$  represents the trait variation independent of both phylogeny and space, defined as  $(1 - \phi)(1 - \lambda_P)$ . Thus, in this model,  $\phi$  will be higher when trait similarities are due to the similar geographical distributions, and spatial effects have a preponderant influence on trait evolution. Conversely,  $\lambda'$  will be higher when close relatives are similar owing to their shared evolutionary history.

The method of Freckleton & Jetz (2009) also allows for the fitting of a linear model on the phylogenetic independent contrasts scaled by the geographic distances among observations, thus accounting for both phylogenetic and spatial dependencies (see also Diniz-Filho *et al.* 2007). We extended their method to perform stepwise model selection, based on the Akaike Information Criterion (AIC). A bidirectional approach was used, in which variables are sequentially removed from the global model, but can be added back in latter steps, mimicking a best subset selection approach (James *et al.* 2013). The three morphological and five environmental variables present in Table 2 composed the global model, also including quadratic terms for Bio01 and Bio28, as well as a multiplicative interaction between these variables. This model was evaluated for each phylogenetic resolution, and the variables excluded by the stepwise selection were sequentially removed from the model. In each step, the variable excluded by the majority of trees was omitted, and the resultant model was reevaluated until the recovery of a model supported by all possible phylogenies. To assess model adequacy, for each tree resolution we compared the final model selected through the stepwise process to a set of null models (Table 3), considering it satisfactory only if supported by all tree resolutions. All variables were transformed to z-scores prior to model fitting. The same global model was used to predict the variation in each echolocation parameter described in Table 1. Given that there is a broad spectrum of frequencies used by bats, the dependent variables were log transformed prior to the analyses. All analyses were conducted on R 3.0.2 (R Core

Team 2013), with the major packages `ape` 3.0-11 (Paradis *et al.* 2004) and `MASS` 7.3-29 (Venables & Ripley 2002).

TABLE 3: Models used to evaluate the variation in echolocation parameters and assess the importance of the phylogenetic and/or spatial components. The global model was subject to the stepwise variable selection (see text), while the four other models comprise the set of null models compared to the final one through AIC.

Model	Parameters	$\lambda'$	$\phi$
Global model	All parameters described in Table 2	Estimated	Estimated
No coefficients	No parameters included	Estimated	Estimated
$\lambda$ only	The final model selected for each echolocation variable	1.00	0.00
$\phi$ only	The final model selected for each echolocation variable	0.00	1.00
Independent	The final model selected for each echolocation variable	0.00	0.00

### 1.3 Results

Overall, echolocation call parameters show a greater proportion of phylogenetic signal over spatial signal (Table 4, Figure 1). Peak frequency, final frequency and call duration show the greatest amount of phylogenetic contribution, and the smallest spatial autocorrelation. Initial frequency has somewhat intermediate estimates of phylogenetic and spatial signals, with overlapping confidence intervals. Removing the species that produce constant frequency calls, in which the initial and peak frequencies are very close or identical, barely changes the estimated initial frequency spatial component ( $\phi = 0.362$ ), and the phylogenetic component suffers just a minor reduction ( $\lambda' = 0.432$ ). Frequency bandwidth, on the other hand, is the only parameter that shows a value of  $\phi$  greater than that of  $\lambda'$ . This parameter also presents the highest independent component  $\gamma$ . The independent component reveals similar estimates of variation independent from

phylogeny and space for the peak, initial and final frequencies, and a lower estimate for call duration.

TABLE 4: Estimates of the relative contribution of the phylogenetic, spatial and independent components in the studied echolocation call parameters. Values represent the median and 95% confidence interval among 100 phylogenetic trees.

Parameter	phylogenetic ( $\lambda'$ )	spatial ( $\phi$ )	independent ( $\gamma$ )
Peak frequency	0.650 (0.55 – 0.75)	0.150 (0.01 – 0.30)	0.201 (0.13 – 0.27)
Initial frequency	0.443 (0.37 – 0.56)	0.365 (0.23 – 0.45)	0.196 (0.15 – 0.23)
Final frequency	0.724 (0.62 – 0.78)	0.057 (0.01 – 0.19)	0.220 (0.16 – 0.25)
Bandwidth	0.200 (0.14 – 0.27)	0.401 (0.24 – 0.50)	0.394 (0.32 – 0.49)
Duration	0.841 (0.80 – 0.87)	0.010 (0.01 – 0.06)	0.147 (0.11 – 0.17)

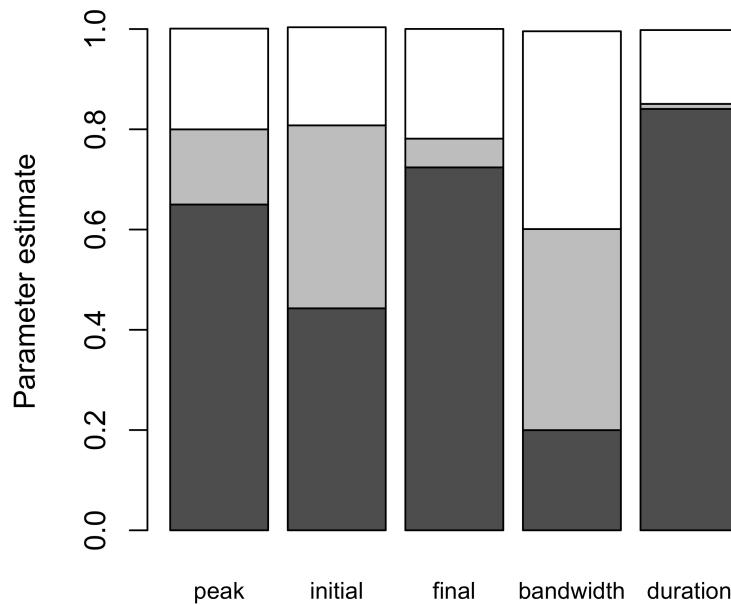


FIGURE 1: Bar charts showing the median values of  $\lambda'$  (dark grey),  $\phi$  (light grey), and  $\gamma$  (white) components estimated for each echolocation call parameter.

Different models were selected for each studied characteristic, showing different relationships between morphological and environmental variables shaping



the variation in these parameters. Among the studied variables, only aspect ratio index was selected as an important variable for all echolocation parameters (Table 5). The results for all four frequency parameters show a consistent pattern of lower frequencies being produced by larger species, as well as those with greater aspect ratio indexes. Call duration, on the other hand, presents an inverse pattern with respect to those two variables.

Amongst environmental variables, annual mean temperature was selected for all call parameters except frequency bandwidth, presenting a pattern of higher frequencies, with low call duration, being produced in regions characterized by high average temperatures. Annual mean moisture was selected only in the models of initial frequency, also with a positive effect. Forest cover, on the other hand, has a negative influence on the initial frequency and a positive effect on call duration. Although frequency bandwidth presented the highest spatial autocorrelation, all environmental variables were discarded following stepwise selection.

TABLE 5: Model coefficients estimated for each echolocation call parameter. Values represent median and 95% confidence interval across phylogenetic tree resolutions. Blank spaces represent variables not included in the final model for the corresponding echolocation parameter. Note that values are in log-linear form.

Call parameter	Aspect ratio index	Forearm length	Tip index	Bio01	Bio28	NDVI
Peak	-0.130 (-0.15 -0.12)	-0.170 (-0.18 -0.16)	0.060 (0.05 0.07)	0.034 (0.03 0.04)		
Initial	-0.228 (-0.25 -0.21)	-0.148 (-0.15 -0.14)		0.046 (0.04 0.05)	0.111 (0.10 0.12)	-0.090 (-0.10 -0.07)
Final	-0.150 (-0.17 -0.14)	-0.196 (-0.20 -0.19)		0.061 (0.06 0.07)		
Bandwidth	-0.438 (-0.46 -0.41)		0.209 (0.19 0.23)			
Duration	0.285 (0.26 0.32)	0.180 (0.17 0.19)	-0.119 (-0.13 -0.10)	-0.103 (-0.11 -0.09)		0.075 (0.07 0.09)

Despite the reasonably high uncertainty in the estimates of the spatial parameter ( $\phi$ ) across trees, for all echolocation call parameters the final models

selected through the stepwise procedure had the smaller AIC value when compared to the considered null models. Even for the call duration parameter, where the median  $\phi$  estimate appears at the lower boundary of this parameter, the model estimating  $\lambda'$  and fixing  $\phi$  at zero was only the third best, with the one estimating both  $\lambda'$  and  $\phi$ , with no variables, appearing as second best for most tree resolutions (Tables S2 to S6).

#### 1.4 Discussion

According to our findings, the four frequency parameters reflect the interplay between environment and phylogenetic history in shaping the variation in echolocation calls. Among these, frequency bandwidth appears as the most plastic and environmentally structured trait, consistent with the background perception task played by the frequency spectrum (Siemers & Schnitzler 2004, Schmieder *et al.* 2012, Denzinger & Schnitzler 2013). The other three frequency parameters show similar estimates of the independent component  $\gamma$ , with peak frequency in between the more spatially structured initial frequency and the more phylogenetically structured final frequency. Call duration, on the other hand, shows the strongest phylogenetic structure, and the smallest independent component. This may be due to the coupling between pulse emission and wing beat in aerial hawking species (Speakman & Racey 1991, Denzinger *et al.* 2004), also shown through the regression coefficients, where the largest animals produce the longest calls (but see Jones 1999). Although the basic call structures are somewhat conserved within families (Jones & Teeling 2006), echolocation features are commonly linked to the habitat in which species forage and commute (Schnitzler & Kalko 2001, Schnitzler *et al.* 2003, Surlykke & Kalko 2008). There is ample variation in habitat use and foraging mode even within families (Denzinger & Schnitzler 2013), and the differences in phylogenetic and spatial signals between parameters show that some features are more adaptable than others in response to the environment.

Various different evolutionary processes and rates can generate similar patterns of phylogenetic signal (Revell *et al.* 2008), but some have stronger impacts than others towards decreasing its estimations, and thus can be disfavored by the results found herein. For example, processes of strong stabilizing selection, punctuated evolution and adaptive radiations may completely erase the signal (Hansen & Martins 1996, Revell *et al.* 2008, Kamilar & Cooper 2013). Behavioral characteristics also commonly bear very low to no phylogenetic autocorrelation (Blomberg *et al.* 2003, Tobias 2011, but see Kamilar & Cooper 2013), and thus the high phylogenetic signal found for most parameters may indicate that the communication role played by echolocation (e.g. Ruczyński *et al.* 2007, 2009) may not be preponderant in the evolution of the biosonar.

The frequency parameters show the expected relationship with body size, with larger animals producing lower frequency calls (Jones 1999, Jacobs *et al.* 2007, Jakobsen *et al.* 2013). Their relation with ambient temperature and moisture seems counterintuitive based on sound attenuation alone, given that higher frequencies are more severely attenuated in warmer and wetter conditions (Lawrence & Simmons 1982, Snell-Rood 2012, Luo *et al.* 2014). High frequencies are associated with the concentration of energy on the second harmonic (Guillen *et al.* 2000), a characteristic found in several species that inhabit the tropical region. Moreover, world's warmer and wetter environments tend to be associated with more dense vegetation (Chapin III *et al.* 2002), in which higher frequencies and broader bandwidths provide more details and directionality to differentiate food items from the surrounding clutter (Lawrence & Simmons 1982, Siemers & Schnitzler 2004, Stilz & Schnitzler 2012, Jakobsen *et al.* 2012, 2013, Denzinger & Schnitzler 2013). However, only the initial frequency showed a consistent relationship with NDVI among all frequency parameters, indicating lower initial frequencies in areas with denser vegetation. This result is consistent with the known positive correlation between wing area and habitat complexity (Fenton 1990, Safi & Dechmann 2005). Longer duration calls provide more information about the background clutter, despite narrowing the prey perception window (Denzinger & Schnitzler 2013), but the positive effect of NDVI on call duration is more probably a consequence of

narrowband callers that fly above the canopy in tropical regions, and thus are not affected by clutter (Griffin 1971, Jung *et al.* 2014).

Bats can dynamically adapt their acoustic beam shape through changes in amplitude and frequency (Surlykke *et al.* 2009, Jakobsen *et al.* 2012, 2013), and several species are known to use different frequencies across their geographic range (e.g. Macias & Mora 2003, Chen *et al.* 2009, Sun *et al.* 2013). These sources of intraspecific variation might weaken the results found herein (see Harmon & Losos 2005, Ives *et al.* 2007), but currently (to the best of our knowledge) there is no available method that estimates both phylogenetic and spatial autocorrelation simultaneously while accounting for intraspecific errors. For instance, estimating Pagel's lambda ( $\lambda_P$ ) accounting for intraspecific errors (see Supplementary Material and Methods) resulted in phylogenetic signals higher than those estimated without intraspecific errors for all characters, with pairwise differences always lower than 0.0015. Given that the geographic centroids do not vary, the estimates of  $\lambda'$  and  $\phi$  including standard errors would probably display a similar effect as found for  $\lambda_P$ , and these minor changes would barely alter the regression coefficients. Taxon sampling, on the other hand, is known to not significantly alter the estimates of phylogenetic signal or correlation coefficients (Ackerly 2000, Freckleton *et al.* 2002, Münkemüller *et al.* 2012), but its impact on the estimation of the spatial signal needs further investigation. Topological errors are another known source of bias in phylogenetic signal estimation, also tending to decrease the signal (Blomberg *et al.* 2003).

In conclusion, our study confirms several proposed relationships between morphology, environment and echolocation, but for the first time using phylogenetically corrected regressions in an analysis comprising all laryngeal echolocating families. Also, we show that the different components of the echolocation pulse have distinct phylogenetic and spatial signals, suggesting that these components play different roles in the environmental perception and food location. The overall preponderance of phylogenetic over the spatial signal does not argue against the role of habitat in shaping the variation in echolocation characteristics. While spatial autocorrelation is measured based on the geographical

distances among species distributions, habitat structuring of echolocation design is based on the distance to vegetation that a species commonly forage (Schnitzler & Kalko 2001, Surlykke & Kalko 2008). Close relatives tend to occupy similar habitats (Villalobos *et al.* 2013), and hence display a high phylogenetic signal even if the spatial autocorrelation was also high (Freckleton & Jetz 2009, Cooper *et al.* 2011). Further analyses are necessary to confirm if the relatively high phylogenetic signal found herein indeed dismiss the role of intraspecific communication in the evolution of echolocation. There is evidence that geographical alterations in echolocation parameters, being it for effective intraspecific communication or self-recognition, is a process that responds to local scale conditions and community composition (Heller & von Helversen 1989, Guillen *et al.* 2000, Russo *et al.* 2007, Sun *et al.* 2013), and in fact no one parameter analyzed can be totally explained by phylogenetic and spatial effects, evidencing this degree of ecological and behavioral plasticity.

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## 1.6 Supplementary material

### Supplementary Material and Methods

Pagel's lambda was estimated across trees with the function `phylosig` from the package `phytools` 0.3-72 (Revell 2012), with and without including the intraspecific standard errors. For each parameter we calculated the mean pairwise difference between the phylogenetic signal estimates across trees.

Revell, L.J. 2012. `phytools`: an R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.* **3**: 217–223.

Table S1: Echolocation parameters available for each species included in the analyses and the respective data sources. Abbreviations refer to: peak frequency (PF), initial frequency (IF), final frequency (FF), bandwidth (BWD) and duration (D). N calls is the combined sample size between studies for each species. References are numbered according to the supplementary references.

Species	PF	IF	FF	BWD	D	N calls	References
<i>Craseonycteris thonglongyai</i>	PF			BWD	D	27	46, 130
<i>Balantiopteryx io</i>	PF	IF	FF	BWD	D	18	49
<i>Balantiopteryx plicata</i>	PF	IF	FF	BWD	D	155	49
<i>Cormura brevirostris</i>	PF	IF	FF	BWD	D	327	33, 59
<i>Cyttarops alecto</i>	PF	IF	FF	BWD	D	123	59
<i>Emballonura monticola</i>	PF	IF	FF	BWD	D	40	108
<i>Peropteryx kappleri</i>	PF	IF	FF	BWD	D	140	59
<i>Peropteryx macrotis</i>	PF	IF	FF	BWD	D	373	9, 15, 79, 115
<i>Rhynchonycteris naso</i>	PF	IF	FF	BWD	D	78	32, 93, 106
<i>Saccolaimus saccolaimus</i>	PF	IF	FF	BWD	D	198	108
<i>Saccopteryx bilineata</i>	PF	IF	FF	BWD	D	479	9, 59, 77, 79, 93, 106
<i>Saccopteryx leptura</i>	PF	IF	FF	BWD	D	329	9, 59, 106
<i>Taphozous georgianus</i>	PF	IF	FF	BWD	D	60	83
<i>Taphozous hildegardae</i>		IF	FF			1	96
<i>Taphozous mauritanus</i>	PF	IF	FF	BWD	D	34	27, 86, 121, 131
<i>Taphozous melanopogon</i>	PF	IF	FF	BWD	D	120	108, 136
<i>Taphozous nudiventris</i>	PF	IF	FF	BWD	D	17	8
<i>Taphozous perforatus</i>	PF	IF	FF	BWD	D	94	7, 8, 33
<i>Furipterus horrens</i>		IF	FF	BWD		1	34, 107
<i>Asellia tridens</i>	PF	IF	FF	BWD	D	38	7, 56
<i>Aselliscus stoliczkanus</i>	PF	IF	FF	BWD	D	16	70, 138
<i>Cloeotis percivali</i>	PF	IF	FF	BWD	D	141	84, 86, 121, 131, 138
<i>Coelops frithii</i>	PF	IF	FF	BWD		21	138
<i>Hipposideros armiger</i>	PF	IF	FF	BWD	D	60	48, 105, 138, 141
<i>Hipposideros ater</i>	PF		FF	BWD	D	54	36
<i>Hipposideros bicolor</i>	PF					56	48, 65, 22
<i>Hipposideros caffer</i>	PF	IF	FF	BWD	D	122	84, 86, 121, 131
<i>Hipposideros cervinus</i>	PF					49	65
<i>Hipposideros cineraceus</i>	PF	IF	FF	BWD	D	117	21, 48, 65, 105
<i>Hipposideros commersoni</i>	PF	IF	FF	BWD	D	153	66
<i>Hipposideros cyclops</i>	PF					1	19
<i>Hipposideros diadema</i>	PF	IF	FF	BWD	D	32	42, 48, 82
<i>Hipposideros fulvus</i>	PF					1	65
<i>Hipposideros galeritus</i>	PF	IF	FF	BWD	D	28	48, 105
<i>Hipposideros larvatus</i>	PF	IF	FF	BWD	D	274	48, 105, 127, 134, 141
<i>Hipposideros lylei</i>	PF	IF	FF	BWD		3	127
<i>Hipposideros pomona</i>	PF	IF	FF	BWD	D	159	22, 105, 127
<i>Hipposideros ruber</i>	PF	IF	FF	BWD	D	449	28, 43, 86
<i>Hipposideros speoris</i>	PF			BWD	D	23	103
<i>Hipposideros turpis</i>	PF					45	48
<i>Rhinonictes aurantia</i>	PF					158	1
<i>Triadenops furculus</i>	PF	IF	FF	BWD	D	153	3, 66
<i>Triadenops persicus</i>	PF	IF	FF	BWD	D	15	86
<i>Cardioderma cor</i>	PF					2	18
<i>Megaderma lyra</i>	PF	IF	FF	BWD	D	36	105, 111
<i>Megaderma spasma</i>	PF	IF	FF	BWD	D	4	105
<i>Miniopterus fraterculus</i>	PF	IF	FF	BWD	D	24	81, 86, 121
<i>Miniopterus inflatus</i>	PF	IF	FF	BWD	D	7	86
<i>Miniopterus manavi</i>	PF	IF	FF	BWD	D	77	66, 110
<i>Miniopterus natalensis</i>	PF	IF	FF	BWD	D	27	81, 86, 121
<i>Miniopterus schreibersii</i>	PF	IF	FF	BWD	D	279	95, 99, 114, 120
<i>Cheiromeles torquatus</i>	PF	IF	FF	BWD	D	84	64
<i>Cynomops planirostris</i>	PF	IF	FF	BWD	D	46	60

<i>Eumops auripendulus</i>	PF	IF	FF	BWD	D	41	60
<i>Eumops bonariensis</i>	PF	IF	FF	BWD	D	8	60
<i>Eumops glaucinus</i>	PF	IF	FF	BWD	D	306	60, 89
<i>Eumops perotis</i>	PF	IF	FF	BWD	D	50	2
<i>Eumops underwoodi</i>	PF	IF	FF	BWD	D	6	97
<i>Molossops mattogrossensis</i>	PF	IF	FF	BWD	D	24	60
<i>Molossops neglectus</i>	PF	IF	FF	BWD	D	28	60
<i>Molossops temminckii</i>	PF	IF	FF	BWD	D	127	44, 60
<i>Molossus molossus</i>	PF	IF	FF	BWD	D	216	15, 60, 94, 106
<i>Molossus rufus</i>	PF	IF	FF	BWD	D	333	15, 31, 33, 60, 79, 94
<i>Molossus sinaloae</i>	PF	IF	FF	BWD	D	203	15, 60, 79, 94, 97
<i>Mormopterus loriae</i>	PF					2	82
<i>Mormopterus minutus</i>	PF	IF	FF	BWD	D	24	88
<i>Mormopterus planiceps</i>	PF	IF	FF	BWD	D	20	37
<i>Nyctinomops laticaudatus</i>	PF	IF	FF	BWD	D	84	15, 60, 79
<i>Nyctinomops macrotis</i>	PF	IF	FF	BWD	D	481	2, 9, 60, 89
<i>Otomops martiensseni</i>	PF	IF	FF	BWD	D	62	29, 121
<i>Promops centralis</i>	PF	IF	FF	BWD	D	12	60
<i>Promops nasutus</i>	PF	IF	FF	BWD	D	30	60
<i>Sauromys petrophilus</i>	PF			BWD	D	61	120, 121
<i>Tadarida aegyptiaca</i>	PF	IF	FF	BWD	D	66	29, 120, 121, 131
<i>Tadarida ansorgei</i>	PF	IF	FF	BWD	D	4	84, 131
<i>Tadarida brasiliensis</i>	PF	IF	FF	BWD	D	350	2, 9, 60, 80, 91, 97, 113
<i>Tadarida chapini</i>	PF	IF	FF	BWD	D	1	131
<i>Tadarida condylura</i>	PF	IF	FF	BWD	D	37	30, 86, 121, 131
<i>Tadarida fulminans</i>	PF	IF	FF	BWD	D	1	27
<i>Tadarida midas</i>		IF	FF	BWD	D	23	30
<i>Tadarida mops</i>	PF	IF	FF	BWD	D	11	64
<i>Tadarida nigeriae</i>		IF	FF	BWD	D	19	30
<i>Tadarida niveiventer</i>	PF			BWD	D	6	121
<i>Tadarida pumila</i>	PF	IF	FF	BWD	D	116	29, 30, 86, 121, 131
<i>Mormoops blainvillei</i>	PF	IF	FF	BWD	D	181	55, 74
<i>Mormoops megalophylla</i>	PF	IF	FF	BWD	D	1503	15, 79, 97, 124
<i>Pteronotus davyi</i>	PF	IF	FF	BWD	D	1921	9, 15, 55, 79, 93, 97, 115, 124
<i>Pteronotus gymnotus</i>	PF	IF	FF	BWD	D	11	50
<i>Pteronotus macleayii</i>	PF	IF	FF	BWD	D	171	74
<i>Pteronotus parnellii</i>	PF	IF	FF	BWD	D	1848	15, 55, 74, 79, 93, 97, 115, 124
<i>Pteronotus personatus</i>	PF	IF	FF	BWD	D	1147	15, 77, 79, 92, 96, 124
<i>Pteronotus quadridens</i>	PF	IF	FF	BWD	D	177	55, 74
<i>Mystacina tuberculata</i>	PF	IF	FF	BWD	D	235	57, 100, 101
<i>Natalus stramineus</i>	PF	IF	FF	BWD	D	17	55, 115
<i>Nyctiellus lepidus</i>	PF	IF	FF	BWD	D	28	91
<i>Noctilio albiventris</i>	PF	IF	FF	BWD	D	3	47, 62
<i>Noctilio leporinus</i>	PF	IF	FF	BWD	D	139	15, 94, 119
<i>Nycteris grandis</i>	PF	IF	FF	BWD	D	34	45, 131
<i>Nycteris macrotis</i>	PF	IF	FF	BWD	D	102	28, 121
<i>Nycteris thebaica</i>	PF	IF	FF	BWD	D	21	84, 120, 121, 131
<i>Nycteris tragata</i>	PF	IF	FF	BWD	D	30	108
<i>Nycteris woodi</i>	PF	IF	FF	BWD	D	1	131
<i>Artibeus cinereus</i>	PF	IF	FF	BWD	D	11	106
<i>Artibeus jamaicensis</i>	PF	IF	FF	BWD	D	101	55, 80, 87, 106
<i>Artibeus lituratus</i>	PF	IF	FF	BWD	D	20	106
<i>Artibeus watsoni</i>	PF	IF	FF	BWD	D	8	41, 67
<i>Brachyphylla cavernarum</i>	PF	IF	FF	BWD	D	4	55
<i>Brachyphylla nana</i>	PF	IF	FF	BWD	D	13	75
<i>Carollia castanea</i>		IF	FF	BWD	D	80	135
<i>Carollia perspicillata</i>	PF	IF	FF	BWD	D	650	12, 106, 135
<i>Centurio senex</i>		IF	FF	BWD	D	1	42
<i>Chiroderma trinitatum</i>	PF	IF	FF	BWD	D	3	106
<i>Chiroderma villosus</i>	PF	IF	FF	BWD	D	4	106
<i>Choeroniscus minor</i>	PF	IF	FF	BWD	D	5	106

<i>Diaemus youngi</i>	PF					1	16
<i>Erophylla bombifrons</i>	PF	IF	FF	BWD	D	5	55
<i>Erophylla sezekorni</i>	PF	IF	FF	BWD	D	11	91
<i>Glossophaga longirostris</i>	PF	IF	FF	BWD	D	8	55
<i>Glossophaga soricina</i>	PF	IF	FF	BWD	D	27	106
<i>Lamproncycteris brachyotis</i>	PF	IF	FF	BWD	D	6	106
<i>Macrophyllum macrophyllum</i>	PF	IF	FF	BWD	D	1012	13, 14, 137
<i>Macrotus californicus</i>		IF	FF	BWD	D	1	6
<i>Macrotus waterhousii</i>	PF	IF	FF	BWD	D	16	91
<i>Micronycteris hirsuta</i>	PF	IF	FF	BWD	D	6	106
<i>Micronycteris megalotis</i>	PF	IF	FF	BWD	D	7	34, 106
<i>Micronycteris minuta</i>	PF	IF	FF	BWD	D	3	106
<i>Mimon bennettii</i>		IF	FF	BWD	D	1	34
<i>Mimon crenulatum</i>	PF	IF	FF	BWD	D	3	106
<i>Monophyllus plethodon</i>	PF	IF	FF	BWD	D	13	55, 80
<i>Phyllonycteris poeyi</i>	PF	IF	FF	BWD	D	88	87
<i>Phyllops falcatus</i>	PF	IF	FF	BWD	D	671	76, 87
<i>Phyllostomus discolor</i>		IF	FF	BWD		1	69
<i>Phyllostomus hastatus</i>	PF	IF	FF	BWD	D	4	61, 106
<i>Platyrrhinus helleri</i>	PF	IF	FF	BWD	D	5	106
<i>Stenoderma rufum</i>	PF	IF	FF	BWD	D	1	55
<i>Sturnira lilium</i>	PF	IF	FF	BWD	D	7	55
<i>Sturnira tildae</i>	PF	IF	FF	BWD	D	5	106
<i>Tonatia saurophila</i>	PF	IF	FF	BWD	D	6	106
<i>Trachops cirrhosus</i>	PF	IF	FF	BWD	D	22	5, 42, 129
<i>Trinycteris nicefori</i>	PF	IF	FF	BWD	D	2	106
<i>Uroderma bilobatum</i>	PF	IF	FF	BWD	D	9	106
<i>Vampyressa pusilla</i>		IF	FF	BWD	D	6	67
<i>Vampyrum spectrum</i>	PF	IF	FF	BWD	D	1	106
<i>Rhinolophus acuminatus</i>	PF					13	48, 65
<i>Rhinolophus affinis</i>	PF	IF	FF	BWD	D	118	48, 65, 105
<i>Rhinolophus alcyone</i>	PF					1	26
<i>Rhinolophus arcuatus</i>	PF					36	122
<i>Rhinolophus beddomei</i>	PF	IF	FF	BWD	D	1	125
<i>Rhinolophus blasii</i>	PF	IF	FF	BWD	D	45	8, 52, 86, 99, 121
<i>Rhinolophus clivosus</i>	PF	IF	FF	BWD	D	91	8, 52, 86, 120, 121
<i>Rhinolophus darlingi</i>	PF	IF	FF	BWD	D	24	52, 86, 121
<i>Rhinolophus deckenii</i>	PF	IF	FF	BWD	D	4	85, 86
<i>Rhinolophus denti</i>	PF					20	52, 121
<i>Rhinolophus euryale</i>	PF	IF	FF	BWD	D	103	99, 114, 116
<i>Rhinolophus ferrumequinum</i>	PF	IF	FF	BWD	D	467	8, 35, 39, 72, 95, 99, 102, 112, 114, 128
<i>Rhinolophus fumigatus</i>	PF				D	5	52, 85, 121
<i>Rhinolophus hildebrandti</i>	PF	IF	FF	BWD	D	26	52, 65, 86, 121
<i>Rhinolophus hipposideros</i>	PF	IF	FF	BWD	D	216	7, 65, 95, 99, 102, 112, 114
<i>Rhinolophus landeri</i>	PF	IF	FF	BWD	D	107	26, 28, 52, 65, 85, 121
<i>Rhinolophus lepidus</i>	PF				D	354	48, 65, 108
<i>Rhinolophus luctus</i>	PF				D	39	48, 65, 108, 138
<i>Rhinolophus macrotis</i>	PF					1	65
<i>Rhinolophus malayanus</i>	PF	IF	FF	BWD	D	245	48, 65, 105, 125
<i>Rhinolophus megaphyllus</i>	PF			BWD	D	29	36
<i>Rhinolophus paradoxolophus</i>	PF					1	24, 138
<i>Rhinolophus pearsonii</i>	PF					10	48, 65
<i>Rhinolophus pusillus</i>	PF	IF	FF	BWD	D	61	48, 65, 105, 138
<i>Rhinolophus rouxii</i>	PF				D	1385	92
<i>Rhinolophus sedulus</i>	PF					9	65
<i>Rhinolophus shameli</i>	PF	IF	FF	BWD	D	121	48, 51, 105
<i>Rhinolophus simulator</i>	PF	IF	FF	BWD	D	26	52, 86, 121
<i>Rhinolophus sinicus</i>	PF					67	138
<i>Rhinolophus steno</i>	PF					137	48, 65, 125, 138
<i>Rhinolophus trifoliatus</i>	PF				D	77	48, 65, 108
<i>Rhinopoma hardwickii</i>	PF	IF	FF	BWD	D	107	33

<i>Rhinopoma microphyllum</i>	PF	IF	FF	BWD	D	10	8, 20
<i>Thyroptera tricolor</i>	PF		FF		D	61	32
<i>Antrozous pallidus</i>	PF	IF	FF	BWD	D	5	27
<i>Barbastella barbastellus</i>	PF	IF	FF	BWD	D	198	95, 102, 112, 114
<i>Chalinolobus gouldii</i>	PF	IF	FF	BWD	D	21	37, 38
<i>Chalinolobus morio</i>	PF	IF	FF	BWD	D	20	37
<i>Chalinolobus picatus</i>	PF					9	104
<i>Chalinolobus tuberculatus</i>	PF	IF	FF	BWD	D	381	100, 101
<i>Corynorhinus townsendii</i>		IF	FF	BWD	D	2	42, 68
<i>Eptesicus brasiliensis</i>	PF	IF	FF	BWD	D	2	106
<i>Eptesicus furinalis</i>	PF	IF	FF	BWD	D	318	79, 94, 115
<i>Eptesicus fuscus</i>	PF	IF	FF	BWD	D	1977	2, 15, 23, 33, 87, 90
<i>Eptesicus hottentotus</i>	PF			BWD	D	16	120, 121
<i>Eptesicus nilssonii</i>	PF	IF	FF	BWD	D	122	35, 95
<i>Eptesicus serotinus</i>	PF	IF	FF	BWD	D	252	95, 99, 102, 112, 114
<i>Glauconycteris variegata</i>	PF			BWD	D	1	121
<i>Hesperoptenus blanfordi</i>	PF	IF	FF	BWD	D	32	64, 105
<i>Histiotus montanus</i>	PF	IF	FF	BWD	D	56	113
<i>Histiotus velatus</i>		IF	FF	BWD	D	1	34, 107
<i>Ia io</i>	PF	IF	FF	BWD	D	4	133
<i>Kerivoula argentata</i>		IF	FF	BWD	D	1	27
<i>Kerivoula lanosa</i>	PF	IF	FF	BWD	D	7	86
<i>Kerivoula papillosa</i>	PF	IF	FF	BWD	D	218	63, 118
<i>Kerivoula pellucida</i>	PF	IF	FF	BWD	D	110	63, 118
<i>Kerivoula picta</i>	PF	IF	FF	BWD	D	271	126
<i>Laephotis angolensis</i>	PF	IF	FF	BWD	D	4	27
<i>Laephotis wintoni</i>	PF		FF	BWD	D	10	54, 121
<i>Lasionycteris noctivagans</i>	PF	IF	FF	BWD	D	678	4, 23, 94
<i>Lasiurus blossevillei</i>	PF	IF	FF	BWD	D	9	15, 58
<i>Lasiurus borealis</i>	PF	IF	FF	BWD	D	1082	17, 23, 90, 91
<i>Lasiurus cinereus</i>	PF	IF	FF	BWD	D	591	4, 23, 38, 94
<i>Lasiurus ega</i>	PF	IF	FF	BWD	D	267	58, 79, 94, 115
<i>Lasiurus intermedius</i>	PF	IF	FF	BWD	D	52	15, 79, 115
<i>Murina aenea</i>	PF	IF	FF	BWD	D	12	63
<i>Murina cyclotis</i>	PF	IF	FF	BWD	D	136	63, 118
<i>Murina leucogaster</i>	PF	IF	FF	BWD	D	190	35, 39, 72, 128
<i>Murina suilla</i>	PF	IF	FF	BWD	D	123	63, 118
<i>Myotis adversus</i>	PF	IF	FF	BWD	D	245	38, 108, 123
<i>Myotis albescens</i>	PF	IF	FF	BWD		1	11
<i>Myotis auriculus</i>	PF	IF	FF	BWD	D	1	123
<i>Myotis austroriparius</i>	PF	IF	FF	BWD	D	486	17
<i>Myotis blythii</i>	PF	IF	FF	BWD	D	201	95, 99, 114
<i>Myotis bocagii</i>	PF	IF	FF	BWD	D	7	86, 121
<i>Myotis californicus</i>	PF	IF	FF	BWD	D	904	40, 94, 123
<i>Myotis chiloensis</i>	PF	IF	FF	BWD	D	67	98, 113
<i>Myotis ciliolabrum</i>	PF	IF	FF	BWD	D	1104	40, 94
<i>Myotis daubentonii</i>	PF	IF	FF	BWD	D	253	95, 99, 102, 112, 114, 117, 128
<i>Myotis evotis</i>	PF	IF	FF	BWD	D	1	42
<i>Myotis frater</i>	PF	IF	FF	BWD	D	20	141
<i>Myotis goudoti</i>	PF	IF	FF	BWD	D	60	66
<i>Myotis grisescens</i>	PF	IF	FF	BWD	D	1588	17, 90
<i>Myotis ikonnikovi</i>	PF	IF	FF	BWD	D	41	35, 128
<i>Myotis keaysi</i>	PF	IF	FF	BWD	D	236	79, 112
<i>Myotis leibii</i>	PF	IF	FF	BWD	D	503	17, 90, 123
<i>Myotis lucifugus</i>	PF	IF	FF	BWD	D	3239	17, 23, 28, 90, 123
<i>Myotis macrodactylus</i>	PF	IF	FF	BWD	D	29	35, 39
<i>Myotis muricola</i>	PF	IF	FF	BWD	D	180	108
<i>Myotis myotis</i>	PF	IF	FF	BWD	D	189	95, 99, 114
<i>Myotis mystacinus</i>	PF	IF	FF	BWD	D	188	95, 99, 102, 112, 114, 123
<i>Myotis nattereri</i>	PF	IF	FF	BWD	D	335	8, 39, 95, 102, 112, 114, 123
<i>Myotis nigricans</i>	PF	IF	FF	BWD	D	867	58, 106, 123



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<i>Myotis riparius</i>	PF	IF	FF	BWD	D	33	32
<i>Myotis ruber</i>		IF	FF	BWD	D	1	123
<i>Myotis septentrionalis</i>	PF	IF	FF	BWD	D	1555	17, 23, 90
<i>Myotis siligorensis</i>	PF			BWD	D	28	130
<i>Myotis sodalis</i>	PF	IF	FF	BWD	D	2846	17, 90
<i>Myotis thysanodes</i>	PF	IF	FF	BWD	D	1	123
<i>Myotis tricolor</i>	PF	IF	FF	BWD	D	25	86, 120, 121, 131
<i>Myotis velifer</i>	PF	IF	FF	BWD	D	41	97
<i>Myotis vivesi</i>		IF	FF	BWD	D	1	10
<i>Myotis volans</i>	PF	IF	FF	BWD	D	2	123
<i>Myotis welwitschii</i>	PF			BWD	D	1	121
<i>Myotis yumanensis</i>	PF	IF	FF	BWD	D	338	94, 97
<i>Nyctalus noctula</i>	PF	IF	FF	BWD	D	398	25, 95, 99, 102, 112, 114
<i>Nycticeinops schlieffeni</i>	PF	IF	FF	BWD	D	33	30, 86, 121
<i>Nycticeius humeralis</i>	PF	IF	FF	BWD	D	298	17, 90
<i>Nyctophilus geoffroyi</i>	PF	IF	FF	BWD	D	21	37, 38
<i>Nyctophilus timoriensis</i>		IF	FF	BWD		16	104
<i>Phoniscus jagorii</i>	PF	IF	FF	BWD	D	20	63, 118
<i>Pipistrellus abramus</i>	PF	IF	FF	BWD	D	210	99, 71
<i>Pipistrellus ariel</i>	PF	IF	FF	BWD	D	290	7, 8
<i>Pipistrellus hesperus</i>	PF	IF	FF	BWD	D	1	42
<i>Pipistrellus kuhlii</i>	PF	IF	FF	BWD	D	314	8, 95, 99, 114
<i>Pipistrellus nanus</i>	PF	IF	FF	BWD	D	137	28, 30, 131
<i>Pipistrellus pipistrellus</i>	PF	IF	FF	BWD	D	362	8, 95, 99, 102, 112, 114, 117
<i>Pipistrellus rueppellii</i>	PF	IF	FF	BWD	D	1	27
<i>Pipistrellus rusticus</i>	PF	IF	FF	BWD	D	48	30, 121, 131
<i>Pipistrellus savii</i>	PF	IF	FF	BWD	D	162	95, 99, 114
<i>Pipistrellus stenopterus</i>	PF	IF	FF	BWD	D	44	64
<i>Pipistrellus subflavus</i>	PF	IF	FF	BWD	D	2514	17, 23, 73, 90
<i>Plecotus auritus</i>	PF	IF	FF	BWD	D	160	95, 112, 114
<i>Plecotus austriacus</i>	PF	IF	FF	BWD	D	393	95, 99, 109, 114, 132
<i>Rhogeessa aeneus</i>	PF	IF	FF	BWD	D	35	79, 115
<i>Rhogeessa io</i>	PF	IF	FF	BWD	D	4	106
<i>Scotoecus albofuscus</i>	PF			BWD	D	1	121
<i>Scotophilus dinganii</i>	PF	IF	FF	BWD	D	52	53, 86, 121
<i>Scotophilus kuhlii</i>	PF	IF	FF	BWD	D	270	108
<i>Scotophilus nigrata</i>	PF	IF	FF	BWD	D	2	27
<i>Scotophilus viridis</i>	PF	IF	FF	BWD	D	29	30, 86
<i>Tylonycteris pachypus</i>	PF	IF	FF	BWD	D	3874	105, 139, 140
<i>Tylonycteris robustula</i>	PF	IF	FF	BWD	D	1976	108, 139, 140
<i>Vespadelus regulus</i>	PF	IF	FF	BWD	D	20	37
<i>Vespertilio sinensis</i>	PF	IF	FF	BWD	D	41	35, 39

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Table S2:  $\Delta AIC$  between the final model (Global model) and the null models fitted to peak frequency on each phylogenetic tree. See Table 3 in the main text for the description of the null models.

Tree	Global model	No coefficients	$\lambda$ only	$\phi$ only	Independent
1	0	84.25	92.25	186.29	151.28
2	0	108.00	116.00	207.46	151.18
3	0	147.95	155.95	202.45	149.25
4	0	93.48	101.48	198.52	147.82
5	0	157.58	165.58	198.04	150.75
6	0	235.16	243.16	191.23	137.86
7	0	63.96	71.96	256.22	142.21
8	0	368.85	376.85	203.33	148.20
9	0	272.24	280.24	214.10	145.22
10	0	134.04	142.04	226.60	146.14
11	0	116.59	124.59	222.29	138.17
12	0	196.50	204.50	237.66	148.58
13	0	179.39	187.39	195.93	142.58
14	0	84.78	92.78	193.90	147.07
15	0	149.67	157.67	191.80	146.19
16	0	110.97	118.97	175.87	148.31
17	0	112.89	120.89	183.00	144.67
18	0	118.05	126.05	184.03	142.94
19	0	146.22	154.22	211.43	152.21
20	0	132.81	140.81	196.10	145.01
21	0	128.37	136.37	200.63	147.91
22	0	130.01	138.01	240.90	144.51
23	0	145.23	153.23	231.75	146.71
24	0	135.09	143.09	238.19	144.00
25	0	61.58	69.58	306.91	147.79
26	0	144.42	152.42	226.87	142.28
27	0	213.80	221.80	231.40	142.56
28	0	199.97	207.97	167.92	150.86
29	0	101.68	109.68	183.71	149.39
30	0	134.77	142.77	210.85	146.14
31	0	179.65	187.65	200.35	151.05
32	0	143.83	151.83	192.98	146.16
33	0	145.26	153.26	168.45	145.86
34	0	228.22	236.22	222.94	143.90
35	0	305.59	313.59	223.86	147.77
36	0	116.78	124.78	225.19	142.23
37	0	147.03	155.03	186.67	144.73
38	0	96.79	104.79	179.96	147.70
39	0	110.33	118.33	214.84	139.52
40	0	87.12	95.12	225.98	145.23
41	0	115.46	123.46	182.87	152.12
42	0	125.99	133.99	184.76	143.82
43	0	135.94	143.94	202.28	145.20
44	0	90.42	98.42	215.39	144.81
45	0	247.58	255.58	170.03	146.36
46	0	127.97	135.97	248.71	151.80
47	0	125.78	133.78	259.52	142.71
48	0	108.55	116.55	299.02	147.40
49	0	80.11	88.11	184.04	143.05
50	0	98.59	106.59	184.50	151.91
51	0	132.03	140.03	190.38	146.77
52	0	168.53	176.53	177.25	144.03
53	0	97.97	105.97	223.22	151.08
54	0	251.16	259.16	210.44	136.79
55	0	80.46	88.46	186.65	145.98
56	0	93.55	101.55	187.21	148.08

57	0	139.50	147.50	269.13	142.93
58	0	125.82	133.82	188.05	143.91
59	0	143.54	151.54	203.44	153.84
60	0	194.86	202.86	258.57	147.72
61	0	187.86	195.86	254.92	147.72
62	0	384.95	392.95	223.87	147.91
63	0	141.26	149.26	196.36	147.89
64	0	176.76	184.76	198.68	149.83
65	0	96.18	104.18	207.99	152.04
66	0	127.02	135.02	238.65	140.63
67	0	120.91	128.91	248.60	140.31
68	0	170.29	178.29	204.54	149.20
69	0	74.05	82.05	166.12	141.10
70	0	124.58	132.58	189.64	144.21
71	0	128.91	136.91	184.24	145.84
72	0	187.09	195.09	258.33	145.10
73	0	96.12	104.12	194.07	144.33
74	0	117.17	125.17	197.99	147.58
75	0	168.99	176.99	178.61	139.13
76	0	120.56	128.56	197.30	146.85
77	0	102.80	110.80	204.60	152.61
78	0	80.38	88.38	232.77	145.87
79	0	101.37	109.37	195.51	157.46
80	0	177.22	185.22	181.24	150.17
81	0	83.87	91.87	195.10	149.13
82	0	86.97	94.97	219.18	146.08
83	0	153.35	161.35	242.64	148.83
84	0	125.68	133.68	186.07	151.49
85	0	209.92	217.92	207.43	145.54
86	0	424.59	432.59	226.42	145.06
87	0	81.50	89.50	200.59	148.01
88	0	100.57	108.57	249.62	153.94
89	0	130.54	138.54	183.88	146.02
90	0	159.28	167.28	187.37	151.06
91	0	174.59	182.59	189.54	149.45
92	0	132.52	140.52	278.55	150.79
93	0	279.13	287.13	257.53	157.11
94	0	148.05	156.05	272.61	152.59
95	0	117.79	125.79	224.80	154.80
96	0	94.28	102.28	177.09	152.05
97	0	191.55	199.55	195.70	153.30
98	0	112.87	120.87	181.94	152.12
99	0	83.79	91.79	189.78	155.96
100	0	177.13	185.13	164.63	153.89

Table S3:  $\Delta\text{AIC}$  between the final model (Global model) and the null models fitted to initial frequency on each phylogenetic tree. See Table 3 in the main text for the description of the null models.

Tree	Global model	No coefficients	$\lambda$ only	$\phi$ only	Independent
1	0	76.93	64.76	116.07	59.34
2	0	80.00	81.12	132.01	67.63
3	0	75.96	103.19	124.23	64.28
4	0	70.57	88.66	122.71	63.67
5	0	70.71	66.29	127.42	64.84
6	0	68.53	70.23	134.53	50.94
7	0	68.98	33.87	120.01	54.52
8	0	69.12	110.01	135.25	60.88
9	0	70.99	246.67	142.99	57.04
10	0	70.30	47.74	114.36	67.18
11	0	71.90	75.60	114.33	62.35
12	0	70.52	216.99	122.34	62.79
13	0	72.55	58.34	144.59	57.55
14	0	72.45	90.75	115.75	62.70
15	0	72.17	106.78	126.76	59.06
16	0	71.64	78.40	114.31	62.54
17	0	69.05	43.15	113.11	62.65
18	0	76.02	71.41	127.68	57.58
19	0	74.06	63.92	148.53	66.79
20	0	77.84	82.51	128.08	63.02
21	0	71.07	72.87	124.07	57.61
22	0	71.44	48.60	119.00	59.58
23	0	67.07	71.61	118.82	65.70
24	0	64.57	98.98	119.07	56.25
25	0	67.79	48.54	118.26	63.97
26	0	71.37	149.78	112.84	57.59
27	0	72.50	58.71	118.93	61.69
28	0	77.89	136.44	155.38	63.94
29	0	68.95	54.10	125.04	63.56
30	0	75.46	65.13	140.86	66.69
31	0	71.17	76.07	126.85	63.31
32	0	71.09	40.66	106.56	60.59
33	0	74.53	63.26	115.48	64.37
34	0	73.31	51.09	116.94	65.60
35	0	75.05	73.10	111.64	67.47
36	0	75.10	88.10	121.50	67.38
37	0	70.76	164.70	109.17	62.89
38	0	70.27	62.94	116.24	63.17
39	0	72.82	50.55	147.86	61.27
40	0	67.78	77.45	148.26	56.73
41	0	70.97	51.77	111.86	62.87
42	0	72.38	79.76	121.09	58.46
43	0	66.00	212.83	132.27	63.32
44	0	69.51	43.51	135.47	65.23
45	0	78.09	61.22	128.71	54.30
46	0	75.72	74.17	125.37	64.39
47	0	81.34	92.78	127.11	61.97
48	0	73.87	44.38	109.77	62.29
49	0	72.27	71.21	117.41	52.18
50	0	74.02	74.78	125.40	64.99
51	0	70.88	93.47	118.14	57.92
52	0	68.52	85.37	132.24	56.29
53	0	68.84	47.47	142.45	61.35
54	0	80.56	78.09	136.62	53.04
55	0	77.39	92.76	117.25	56.78
56	0	77.22	72.23	126.85	53.03

57	0	72.18	72.05	134.66	51.05
58	0	69.27	49.41	124.26	52.26
59	0	73.59	85.59	112.31	65.69
60	0	75.12	63.58	132.46	67.71
61	0	75.66	84.87	121.19	63.56
62	0	80.37	123.19	112.35	66.17
63	0	73.50	61.98	118.67	59.42
64	0	74.89	224.65	138.81	57.87
65	0	66.63	76.54	123.45	58.57
66	0	74.76	64.14	122.44	58.51
67	0	82.60	46.32	130.67	56.69
68	0	72.51	167.03	127.46	62.75
69	0	75.68	116.96	112.48	58.89
70	0	70.94	53.52	118.15	54.22
71	0	70.92	78.84	127.05	62.02
72	0	70.40	122.53	128.45	61.97
73	0	69.83	63.19	153.27	56.93
74	0	73.62	107.26	134.30	61.88
75	0	73.97	62.36	127.80	60.74
76	0	70.03	85.32	125.13	62.59
77	0	69.25	78.99	118.80	65.39
78	0	71.49	82.79	126.13	56.86
79	0	72.11	188.76	108.53	65.74
80	0	71.98	65.73	115.83	61.75
81	0	68.02	93.81	118.29	60.55
82	0	74.38	69.60	148.70	59.72
83	0	73.81	89.98	118.22	67.57
84	0	68.56	67.18	127.89	64.54
85	0	63.86	73.46	145.32	58.66
86	0	67.72	56.39	137.92	59.47
87	0	71.24	69.98	131.03	55.68
88	0	80.00	89.98	124.07	66.07
89	0	74.46	75.88	132.71	58.71
90	0	73.27	77.99	123.74	62.42
91	0	71.34	48.14	122.19	70.03
92	0	65.66	53.89	146.70	64.13
93	0	73.83	125.74	117.90	64.68
94	0	77.88	111.48	142.50	69.68
95	0	73.03	61.19	155.47	66.34
96	0	72.26	104.60	119.95	66.42
97	0	73.69	75.09	125.72	66.99
98	0	72.18	116.93	115.29	61.87
99	0	75.43	69.61	125.42	60.21
100	0	74.64	38.87	112.90	67.66

Table S4:  $\Delta\text{AIC}$  between the final model (Global model) and the null models fitted to final frequency on each phylogenetic tree. See Table 3 in the main text for the description of the null models.

Tree	Global model	No coefficients	$\lambda$ only	$\phi$ only	Independent
1	0	95.37	51.78	167.47	131.00
2	0	97.84	48.08	182.52	135.79
3	0	92.01	112.65	182.03	128.90
4	0	83.92	64.17	179.31	128.36
5	0	84.01	91.06	179.63	128.48
6	0	85.96	86.06	187.25	123.68
7	0	85.15	76.40	177.39	125.62
8	0	84.21	89.56	183.00	128.15
9	0	84.96	102.34	183.53	130.42
10	0	86.70	120.14	166.30	127.23
11	0	84.69	145.40	167.42	119.19
12	0	89.59	126.51	192.49	126.36
13	0	90.60	64.21	182.90	125.23
14	0	88.64	46.06	186.64	126.97
15	0	85.83	88.97	179.66	126.18
16	0	88.90	250.67	163.87	128.73
17	0	79.62	113.92	172.96	123.16
18	0	89.07	97.47	174.99	128.29
19	0	87.67	41.65	226.64	135.71
20	0	90.98	56.01	186.44	133.94
21	0	84.90	139.64	181.38	125.56
22	0	87.06	59.12	181.20	128.17
23	0	80.84	54.01	182.03	132.25
24	0	78.93	41.72	183.14	129.26
25	0	81.63	62.87	184.64	128.32
26	0	84.70	94.58	182.75	126.78
27	0	85.02	302.68	177.49	122.27
28	0	89.39	48.10	151.60	131.62
29	0	82.99	53.95	176.68	126.83
30	0	86.63	101.79	211.49	128.03
31	0	85.51	73.13	172.03	126.48
32	0	89.87	46.22	176.13	127.03
33	0	87.49	106.18	173.15	123.70
34	0	85.38	119.29	156.86	126.25
35	0	90.06	42.20	158.05	130.46
36	0	86.01	61.64	186.81	127.76
37	0	85.17	133.45	179.31	127.52
38	0	86.48	127.79	157.39	127.31
39	0	85.27	63.15	216.23	120.75
40	0	84.47	54.85	219.54	124.33
41	0	84.30	60.14	172.86	122.51
42	0	88.71	63.12	177.15	124.37
43	0	82.81	114.59	188.30	127.31
44	0	81.14	47.91	217.40	129.46
45	0	90.68	54.89	153.18	131.90
46	0	90.02	121.41	170.61	135.08
47	0	89.40	87.49	188.25	127.34
48	0	87.88	49.77	174.27	126.15
49	0	87.51	85.81	163.96	128.10
50	0	88.62	92.43	182.31	131.43
51	0	86.07	72.16	182.03	131.23
52	0	81.90	95.94	177.78	126.19
53	0	83.16	105.97	222.66	129.68
54	0	93.41	126.61	221.39	129.42
55	0	92.26	48.92	174.29	126.14
56	0	93.75	89.05	174.64	126.75

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57	0	92.29	85.81	195.72	127.96
58	0	88.28	85.95	177.66	122.44
59	0	90.34	268.23	180.33	128.79
60	0	92.19	63.36	171.42	130.38
61	0	90.89	228.33	180.40	128.62
62	0	89.27	226.57	159.66	126.63
63	0	92.40	45.48	179.69	128.43
64	0	95.14	130.83	186.31	130.86
65	0	85.99	58.64	198.88	129.28
66	0	91.11	77.39	195.15	125.72
67	0	92.17	39.37	197.87	126.43
68	0	87.15	153.99	179.64	124.97
69	0	88.88	66.80	151.68	125.64
70	0	88.12	115.95	185.44	125.14
71	0	85.82	57.31	166.03	128.88
72	0	80.11	76.43	196.86	129.81
73	0	86.64	45.83	195.97	128.98
74	0	88.28	46.68	197.70	125.58
75	0	86.78	55.91	165.65	124.96
76	0	86.65	131.93	164.89	124.10
77	0	84.92	94.61	180.17	128.77
78	0	86.23	121.87	171.42	128.46
79	0	87.55	86.12	160.53	132.61
80	0	85.56	55.32	175.16	128.01
81	0	86.14	43.49	187.40	130.94
82	0	89.73	75.68	231.02	126.53
83	0	85.73	130.89	184.25	127.25
84	0	85.02	47.43	187.49	133.36
85	0	83.86	69.79	208.67	133.10
86	0	87.07	86.94	198.70	128.33
87	0	87.87	61.97	170.08	125.99
88	0	92.27	107.77	182.20	128.49
89	0	90.16	120.77	202.49	123.79
90	0	84.76	43.87	178.90	128.11
91	0	84.41	52.35	178.21	127.90
92	0	84.48	47.68	223.76	126.99
93	0	89.18	287.34	178.35	127.98
94	0	88.20	66.50	213.17	128.96
95	0	88.91	44.97	234.12	131.88
96	0	86.83	76.37	165.94	128.27
97	0	88.53	77.72	185.01	130.05
98	0	87.70	114.44	164.92	127.08
99	0	91.18	165.95	182.55	127.44
100	0	91.08	73.74	146.54	129.58

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Table S5:  $\Delta AIC$  between the final model (Global model) and the null models fitted to frequency bandwidth on each phylogenetic tree. See Table 3 in the main text for the description of the null models.

Tree	Global model	No coefficients	$\lambda$ only	$\phi$ only	Independent
1	0	15.94	164.17	141.49	68.81
2	0	15.91	164.05	148.97	70.59
3	0	18.11	219.50	153.76	65.44
4	0	16.61	240.04	150.09	65.37
5	0	16.00	159.10	160.63	65.54
6	0	15.33	258.96	154.09	62.77
7	0	17.25	202.81	161.53	59.89
8	0	17.27	330.49	155.18	66.74
9	0	17.81	541.74	190.17	64.03
10	0	15.88	202.22	168.42	62.73
11	0	14.67	364.73	170.68	62.80
12	0	16.62	304.66	158.74	57.21
13	0	12.80	128.29	149.50	64.09
14	0	15.77	197.70	151.11	65.66
15	0	19.78	236.42	143.83	65.17
16	0	16.98	439.43	173.66	57.61
17	0	14.69	188.74	146.68	61.14
18	0	20.67	186.60	174.62	62.63
19	0	13.84	150.65	147.67	69.88
20	0	17.46	139.53	163.41	68.60
21	0	14.55	206.36	182.38	63.24
22	0	17.17	285.50	167.84	65.41
23	0	15.32	161.02	163.79	63.35
24	0	16.19	231.40	178.17	59.12
25	0	13.74	147.09	159.46	65.42
26	0	16.72	240.39	157.10	59.62
27	0	18.13	173.09	145.93	65.86
28	0	18.25	260.15	159.05	60.20
29	0	14.81	164.05	164.28	65.53
30	0	16.40	210.75	168.46	67.49
31	0	13.59	161.70	146.49	69.76
32	0	15.94	150.94	165.93	60.33
33	0	14.98	205.85	155.97	63.84
34	0	12.58	150.01	173.72	67.85
35	0	14.28	243.86	158.37	65.69
36	0	15.72	165.08	163.84	65.21
37	0	13.81	211.09	145.45	64.69
38	0	15.04	110.78	164.50	58.66
39	0	15.98	165.91	166.11	65.54
40	0	17.22	224.53	169.56	64.10
41	0	17.41	160.84	153.31	61.45
42	0	18.75	167.42	180.97	61.86
43	0	16.43	281.92	146.10	67.41
44	0	16.41	132.17	182.17	61.61
45	0	17.66	184.26	180.79	63.75
46	0	18.74	177.34	159.85	66.02
47	0	20.23	226.16	148.34	65.91
48	0	16.40	113.19	157.88	64.00
49	0	18.42	154.32	168.22	63.20
50	0	14.15	137.91	167.65	68.23
51	0	15.34	178.76	158.55	62.60
52	0	17.20	213.19	160.69	63.02
53	0	15.78	264.45	164.15	64.50
54	0	15.79	209.08	152.73	63.57
55	0	18.15	185.37	164.71	63.86
56	0	15.93	222.03	152.88	61.44



57	0	17.73	345.00	166.98	56.68
58	0	15.86	176.95	174.50	61.65
59	0	16.55	300.78	140.09	64.93
60	0	15.15	168.22	145.81	69.53
61	0	17.01	186.20	147.54	73.00
62	0	16.84	553.72	146.56	66.38
63	0	15.38	130.27	152.93	67.35
64	0	13.52	327.54	149.96	65.05
65	0	14.78	130.45	146.16	63.52
66	0	16.69	144.77	163.14	65.34
67	0	20.69	120.70	161.06	69.47
68	0	15.33	225.18	163.87	67.80
69	0	15.91	227.90	146.06	65.76
70	0	17.92	125.78	191.89	65.03
71	0	16.17	178.05	186.88	61.99
72	0	15.68	316.37	188.61	65.05
73	0	14.62	128.61	206.81	62.43
74	0	13.25	215.18	148.08	63.82
75	0	14.39	145.91	151.15	68.30
76	0	13.85	175.32	153.34	65.50
77	0	14.29	155.55	169.08	67.92
78	0	17.37	299.86	174.56	63.29
79	0	14.76	366.69	157.44	66.92
80	0	15.17	201.20	167.17	66.68
81	0	13.92	158.63	149.04	64.85
82	0	16.24	165.85	172.01	63.12
83	0	16.89	163.46	157.88	68.38
84	0	14.36	163.40	150.53	67.23
85	0	14.48	188.24	157.53	64.15
86	0	11.60	158.98	149.72	69.69
87	0	14.55	260.62	157.03	68.24
88	0	16.21	116.78	152.63	73.16
89	0	13.74	158.51	140.65	68.21
90	0	14.54	221.58	147.24	69.20
91	0	13.10	148.50	147.66	69.67
92	0	12.70	129.61	140.90	66.64
93	0	15.00	261.64	152.37	65.04
94	0	16.24	242.99	167.81	64.16
95	0	14.53	160.73	160.80	65.35
96	0	13.46	147.16	146.07	67.61
97	0	13.53	229.69	137.54	69.88
98	0	17.41	162.01	149.01	62.70
99	0	17.19	207.65	144.75	68.14
100	0	16.96	206.11	147.39	62.14

Table S6:  $\Delta\text{AIC}$  between the final model (Global model) and the null models fitted to call duration on each phylogenetic tree. See Table 3 in the main text for the description of the null models.

Tree	Global model	No coefficients	$\lambda$ only	$\phi$ only	Independent
1	0	60.25	38.27	169.03	292.23
2	0	55.63	65.51	169.97	284.02
3	0	57.67	27.92	149.45	288.38
4	0	55.35	36.72	165.96	286.98
5	0	52.29	42.13	160.53	281.53
6	0	51.71	71.04	167.08	276.13
7	0	56.32	49.92	186.21	280.57
8	0	55.44	95.36	167.77	278.82
9	0	56.35	66.86	164.07	281.56
10	0	56.28	65.31	176.36	283.02
11	0	56.60	128.53	169.90	282.87
12	0	53.19	233.13	147.79	279.60
13	0	53.33	64.18	169.39	282.62
14	0	53.46	69.20	150.51	280.08
15	0	58.54	115.57	160.66	284.69
16	0	57.25	67.41	180.56	288.83
17	0	55.64	64.90	149.01	282.55
18	0	59.74	59.97	182.50	286.20
19	0	56.68	48.35	157.29	286.64
20	0	56.03	40.63	178.54	279.27
21	0	58.94	111.56	165.00	283.31
22	0	56.57	65.17	151.63	283.83
23	0	58.83	92.63	168.52	284.30
24	0	56.07	60.63	162.44	281.42
25	0	56.84	42.15	192.47	284.67
26	0	54.58	127.81	140.95	276.76
27	0	57.24	132.92	150.55	282.78
28	0	59.80	60.15	167.69	286.23
29	0	58.23	53.62	176.73	282.31
30	0	62.48	80.07	175.03	287.14
31	0	62.26	35.75	156.50	292.44
32	0	58.26	26.21	176.64	287.05
33	0	58.52	43.82	175.07	290.41
34	0	58.69	126.29	153.29	285.49
35	0	53.20	83.19	179.43	282.06
36	0	53.84	148.80	192.29	285.73
37	0	53.04	112.54	146.37	283.52
38	0	57.48	30.52	182.36	289.34
39	0	57.09	46.21	180.85	284.57
40	0	56.01	43.49	151.49	280.91
41	0	50.96	72.48	170.26	282.81
42	0	56.93	40.17	162.10	287.00
43	0	58.05	255.47	175.40	287.05
44	0	58.23	69.15	167.79	280.79
45	0	62.50	58.97	174.95	283.62
46	0	61.65	122.98	165.15	283.19
47	0	58.51	59.03	143.28	282.05
48	0	54.63	58.50	170.37	283.21
49	0	56.60	77.58	167.60	283.54
50	0	57.25	39.51	168.25	282.80
51	0	57.14	58.40	149.92	283.51
52	0	57.53	50.97	175.02	281.69
53	0	57.28	82.68	147.44	279.86
54	0	60.11	23.98	179.20	279.82
55	0	57.42	34.23	169.26	280.78
56	0	56.11	42.63	157.17	284.16

57	0	54.50	294.83	155.43	277.70
58	0	52.88	38.79	181.57	281.72
59	0	58.34	153.76	148.13	280.58
60	0	57.79	74.67	165.03	278.95
61	0	59.85	139.62	164.11	285.96
62	0	59.38	77.09	152.57	284.35
63	0	55.36	76.22	169.01	279.84
64	0	57.69	154.65	182.66	287.01
65	0	52.09	70.90	151.87	283.50
66	0	55.20	38.23	166.26	278.44
67	0	62.28	21.51	167.60	280.08
68	0	54.33	134.69	181.11	284.25
69	0	54.80	71.95	195.01	285.90
70	0	62.09	124.43	158.39	281.49
71	0	53.10	45.73	173.34	283.89
72	0	51.27	99.94	155.31	286.26
73	0	54.72	37.25	160.82	283.02
74	0	58.50	71.06	176.48	283.26
75	0	54.59	82.69	174.39	281.56
76	0	51.04	64.71	171.53	284.44
77	0	53.76	60.43	160.52	284.80
78	0	57.79	70.56	177.81	288.70
79	0	54.61	121.09	174.18	286.89
80	0	55.93	90.57	151.60	285.73
81	0	57.24	38.45	151.18	284.40
82	0	56.69	28.60	156.74	283.74
83	0	56.05	92.72	172.65	282.63
84	0	55.74	61.92	163.61	288.01
85	0	53.88	34.44	161.86	281.66
86	0	57.64	52.58	174.17	284.19
87	0	58.46	66.80	165.48	279.65
88	0	57.77	33.34	151.97	280.46
89	0	54.87	61.19	176.65	279.88
90	0	58.53	57.30	168.54	283.07
91	0	57.25	40.48	152.74	281.13
92	0	52.97	55.30	170.16	281.55
93	0	55.73	63.50	157.32	281.71
94	0	60.37	68.13	174.03	281.44
95	0	55.25	45.58	193.32	279.68
96	0	62.79	38.09	196.51	283.57
97	0	59.13	70.11	154.24	288.02
98	0	57.02	82.89	164.96	283.56
99	0	56.48	94.87	178.67	279.42
100	0	54.20	97.29	171.98	279.12

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## **CAPÍTULO 2**

### **THE TEMPO OF ECHOLOCATION EVOLUTION**

## 2.1 Introduction

Powered flight and echolocation are probably the main keys to the exceptional diversity of bats (Simmons 2005, Jones & Teeling 2006). Almost 85% of all known bat species are capable of echolocating through sounds produced in their larynx (Schuller & Moss 2004), an active process that enables them to navigate and forage in the dark (Griffin 1946, Griffin *et al.* 1960, Korine & Kalko 2005). Several studies dealt with the question of whether echolocation or flight appeared first (e.g. Fenton *et al.* 1995, Norberg 1994, Speakman 1993, reviewed in Denzinger *et al.* 2004), as well as whether echolocation evolved once or twice (Teeling *et al.* 2000, 2005, Eick *et al.* 2005, Teeling 2009). Recently this debate was reinforced by the discovery of a form of echolocation based on wing clicks in species from three distant subfamilies within Pteropodidae (Boonman *et al.* 2014), in which only one genus was known to echolocate by means of tongue clicks (Yovel *et al.* 2010). This process, however, is different from the tonal calls produced in the other 18 bat families (Boonman *et al.* 2014, Fenton & Ratcliffe 2014). Despite the number of studies dealing with the origin of echolocation, the dynamics of its evolution within the laryngeal echolocating bats is still poorly understood.

Tonal bat echolocation (hereafter ‘echolocation’) is produced in a variety of call types or “shapes” that depict the relationship between call frequency and duration (Neuweiler 1989, Jones & Holderied 2007), with some remarkable cases of convergence of call types among distantly related groups (Jones & Teeling 2006, Maltby *et al.* 2012). The most conspicuous differentiation – between high (HDC) and low duty-cycle (LDC) echolocation (Fenton *et al.* 1995, 2012) – describes the relationship between call duration and interval, dividing the majority of species that use LDC and separate echoes in time (Kalko & Schnitzler 1989) from the HDC species, which emit long constant frequency calls separated by short intervals and are capable of discriminate echoes based on frequency alterations rather than time (Bell & Fenton 1984). HDC also represents the most prominent case of call type convergence, with the presence of HDC echolocation in two families from the Old World Rhinolophoidea and in one distantly related species from the New World,

*Pteronotus parnellii*. More generally, call types can be differentiated according to the amplitude of frequencies spanned within a call (Schnitzler *et al.* 2003), basically dividing bats in broadband, narrowband and constant frequency echolocators, which in turn are subdivided based on harmonic composition and call intensity (Jones & Teeling 2006).

Call types can be associated with the range and directionality of echolocation (Holderied *et al.* 2006, Jones & Holderied 2007), and bats can adjust multiple call and behavioral parameters to suitably probe the environment (Holderied & von Helversen 2003, Jakobsen *et al.* 2012, 2013). Consequently, differences in call structure are assumed to have a close relationship with the primary habitats occupied by the species (Schnitzler & Kalko 1998, 2001, Schnitzler *et al.* 2003, Surlykke & Kalko 2008). Narrowband signals are mainly associated with open habitats. Characterized by low frequency and high intensity (Jung *et al.* 2014), these calls can span for long distances and are best suited to the capture of insects in flight. The use of multiple harmonics within this type of call can be associated with hunting in open space close to vegetation or water streams (Jung *et al.* 2007). Broadband signals, on the other hand, are best suited for locating prey surrounded by clutter. In this type of call, a wide range of frequencies are covered within short time intervals (Schnitzler *et al.* 2003, Jones & Teeling 2006) guaranteeing a more precise time determination of echo return, facilitating the differentiation between prey items and the background (Moss & Surlykke 2010). The inclusion of higher harmonics within broadband signals provides information about the background that differs in frequency from those of the harmonic with most energy (Bates & Simmons 2010, Bates *et al.* 2011). Constant frequency HDC echolocation is probably the most specialized form of echolocation (Fenton *et al.* 2012). These species commonly occupy narrow space habitats and prey on moving insects (Jones & Teeling 2006), being capable of differentiate prey sizes based on the frequency alterations caused by the insect's wing-beating (Emde & Schnitzler 1990, Koselj *et al.* 2011).

In addition to the relation with habitat use and foraging mode, echolocation has an intrinsic relationship with body size (Aldridge & Rautenbach 1987, Norberg

& Rayner 1987). Call frequency is inversely scaled with forearm length (Jones 1999, Bilski *et al.* – Chapter 1), a property that confers a similar sonar beam shape ('field of view') to disparately sized species (Jakobsen *et al.* 2012). Call emission has an energetic cost as high as powered flight (Speakman *et al.* 1989), but through coupling its emission with wing beating, this elevated energy requirement is cancelled (Speakman & Racey 1991, Voigt & Lewanzik 2012). However, in LDC species, the emission rate must be adjusted to avoid the masking of successive calls and returning echoes (Schnitzler & Kalko 2001, Schintzler *et al.* 2003), a task that depends on the call frequency and intensity, and its attenuation through the atmosphere (Lawrence & Simmons 1982). To avoid this masking, larger species, which emit lower frequency calls, tend not to call at every wing beating (Holderied & von Helversen 2003). The frequency of maximum energy and the forearm length, thereby, may reflect the relationship between the extrinsic and intrinsic forces that shape the biosonar. However, determining how this allometric scaling and the habitat structuring of echolocation design affects the pace of phenotypic evolution and translates into different rates of frequency and size differentiation among clades, is an open question.

Describing the tempo of phenotypic evolution, the rate at which variance accumulates through time, is essential for understanding how it is produced and maintained (Adams 2013), and the adoption of an explicit phylogenetic context is paramount in the comparison of phenotypic variances among related groups (O'Meara *et al.* 2006, Adams *et al.* 2009). Rates of phenotypic evolution can vary among clades due to geographical isolation (Harmon *et al.* 2008, Wiens *et al.* 2011), as well as differences in morphological (Puttick *et al.* 2014), ecological (Thomas *et al.* 2009, Davis *et al.* 2014, Kaliontzopoulou *et al.* 2015) and behavioral characteristics (Thomas *et al.* 2006). The ecological release associated with the colonization of a different habitat or niche dimension (Mahler *et al.* 2010, Yoder *et al.* 2010) is commonly associated with the acceleration in rates of diversification (Losos & Miles 2002, Alfaro *et al.* 2009) and phenotypic differentiation. Despite that, Harmon *et al.* (2010) found little evidence for adaptive radiations (or 'early bursts') of morphological disparity in several animal taxa (not including Chiroptera),

implying that characters continue to differentiate after the species diversification reaches some equilibrium (Rabosky & Lovette 2008, Yoder *et al.* 2010). Hence, differences in ecological conditions and bursts of lineage diversification do not necessarily lead to different rates of phenotypic evolution.

In this paper, we aim to investigate if the different types of echolocation are associated with different rates of phenotypic evolution of frequency of maximum energy and forearm length. Moreover, we aim to examine if the convergence of echolocation types leads to convergent rates of evolution among groups that echolocate in the same manner. We investigate that through a series of hypotheses of phenotypic differentiation among and within clades. For ease of interpretation, we accounted for different rates only within a Brownian motion model of evolution (Felsenstein 1985, Pagel 1999, Freckleton *et al.* 2002), with multiple rates (O'Meara *et al.* 2006, Thomas *et al.* 2006). Although this model is often taken to represent just a process of neutral evolution (Butler & King 2004), other processes like directional selection towards a varying optima and punctuated evolution are also appropriately modeled by a Brownian motion model (Hansen & Martins 1996, O'Meara *et al.* 2006). Although the use of evolutionary models based on the Ornstein-Uhlenbeck process, which directly specify the presence and attraction to selective regimes (Hansen 1997), appears more compelling, Ho & Ané (2014) recently revealed problems associated with the maximum likelihood estimation of its parameters, and the preference for this model in data driven approaches may be more a statistical property of large datasets than a real biological attribute (Pennell *et al.* 2014a).

## 2.2 Material and Methods

We gathered data on echolocation calls of 372 bats species (39% of the echolocating bat species according to Wilson & Reeder 2005. See supplementary Table S1 for a description of the dataset representativeness) from published articles, field guides and theses (see supplementary Table S2 for the references



used). Only calls explicitly measured during the search phase (Griffin *et al.* 1960) were used. For species with more than one data source, we computed weighted averages considering the number of calls reported in each source, assuming it to be one single call when this information was absent. Forearm lengths of these species were collected at the Royal Ontario Museum mammalian collection, supplemented with data from the PanTHERIA database (Jones *et al.* 2009).

The most complete bat phylogeny to date is part of the mammalian supertree of Bininda-Emonds *et al.* (2007, 2008). Although Fritz *et al.* (2009) updated and corrected this supertree species nomenclature based on Wilson & Reeder (2005), we still found 61 cases of incorrect bat species names, and manually corrected them throughout the phylogeny. This tree, however, is only 51% resolved, so we used 100 time-calibrated trees randomly sampled from the Bayesian pseudo-posterior distribution of trees provided by Kuhn *et al.* (2011) to build a maximum clade credibility tree (hereafter *mccTree*) using the program *TreeAnnotator* 1.7.5 from the *Beast* software package (Drummond *et al.* 2012).

We evaluated 18 hypotheses of differential rates of evolution of frequency of maximum energy (FME) using the R package *OUwie* 1.4.4 (Beaulieu *et al.* 2012), under a Brownian motion model of evolution (see O'Meara *et al.* 2006 for a full description of this approach, and also Thomas *et al.* 2006). The null hypothesis of a single homogeneous rate across all clades was tested against alternative hypotheses based on the classification of echolocation types made by Jones & Teeling (2006), which categorize bats in eight categories based on the general structure of their echolocation calls. Although they recognize that these categories are not representative of all species in any given family, arguing that they can vary according to habitat and specific behaviors, we here consider these structures to be ubiquitous among species within most families, except *Mormoopidae* and *Vespertilionidae*. Variations within families are, at least to some extent, captured by the different evaluated hypotheses.

In the initial scenario, H1, all species within each family were classified in one of the following categories: constant frequency – CF; narrowband multiharmonic –

NM; short, broadband multiharmonic – SBM; narrowband fundamental harmonic – NF; short, broadband, fundamental harmonic - SBF; and polymorphic – P (see Jones & Teeling 2006 for the full call structure descriptions). The polymorphic classification adopted herein comprises those species that intermingle frequency modulated and constant frequency portions within a call, namely Noctilionidae and Mormoopidae – with the exception of *Pteronotus parnellii*, which was classified as CF. For Vespertilionidae, we classified most members as SBF, and those species in which the initial frequency is less than one octave higher than the final frequency (Schnitzler & Kalko 2001) were classified as NF. The other 16 hypothetical scenarios were composed of simplifications of this classification (Figure 1, Table 1), aggregating species and families according to the reconstructed ancestral states of the clades to which they pertain, and also a simpler classification differing bats into HDC and LDC callers (Fenton *et al.* 1995, Fenton 2012).

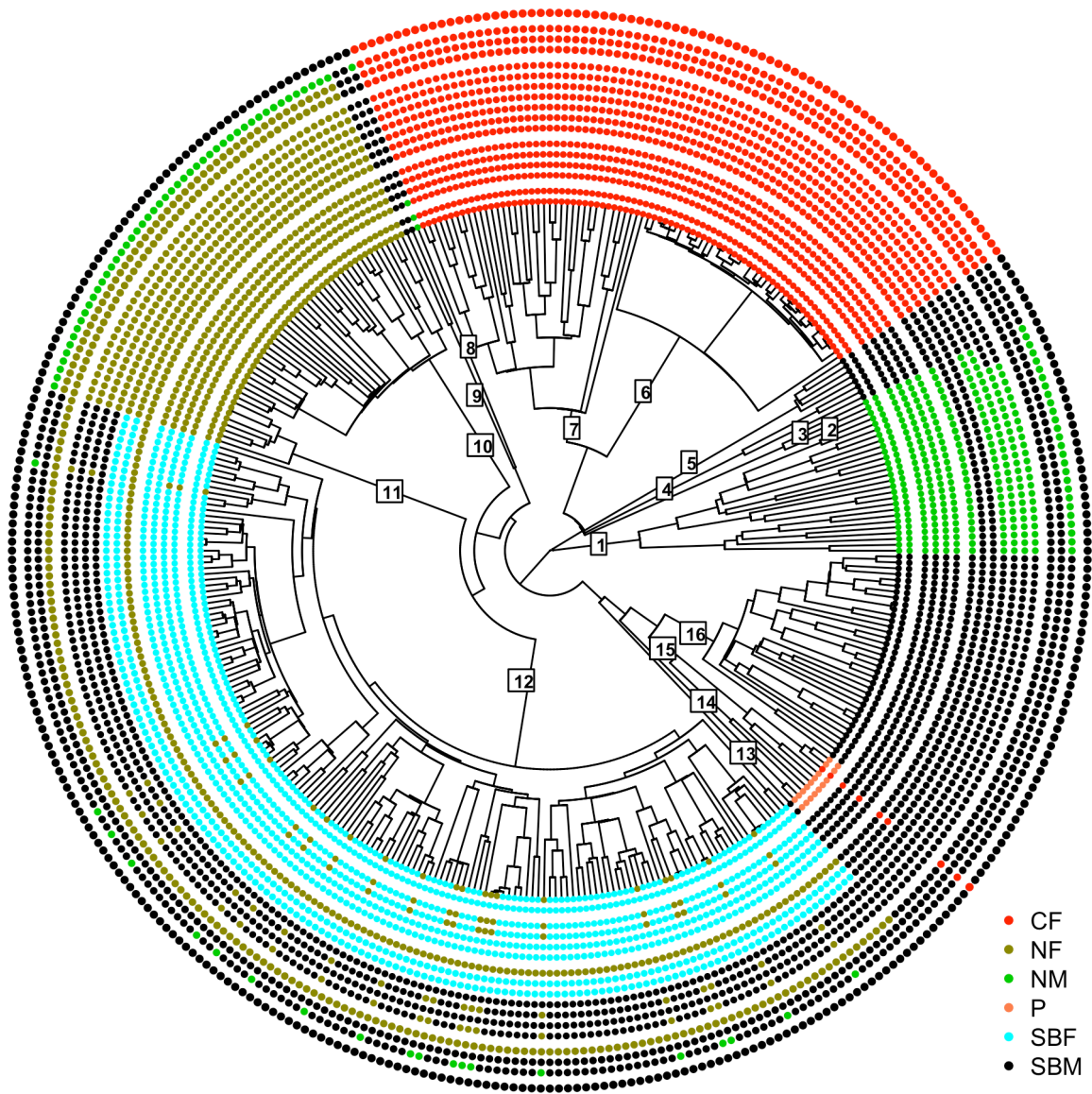


Figure 1: Maximum clade credibility tree depicting the 17 hypothesis of differential rates of evolution across the different types of call structure. The innermost circle depicts the most comprehensive hypothesis, H1, with six rates of evolution, while the other circles represent simplifications of the first scenario. The outermost circle is the hypothesis of two rates, separating HDC and LDC species (H17). Sets of hypotheses are separated with blank spaces according to the number of putative rates (see Tables 1 and 2). Numbers along branches represent the 16 families analyzed: 1-Emballonuridae, 2-Craseonycteridae, 3-Rhinopomatidae, 4-Megadermatidae, 5-Nycteridae, 6-Rhinolophidae, 7-Hipposideridae, 8-Thyropteridae, 9-Natalidae, 10-Molossidae, 11-Miniopteridae, 12-Vespertilionidae, 13-Mystacinidae, 14-Noctilionidae, 15-Mormoopidae, 16-Phyllostomidae. See the supplementary figure S1 for the mappings of each hypothesis into the phylogeny.

Table 1: Call structure classification assumed for each family in the 18 hypotheses of differential rates of phenotypic evolution. The first scenario, BM1, assumes a single rate of evolution for all call types. H1 refers to the six call structures described in Jones & Teeling (2006), while the other hypotheses represent simplifications of this first scenario (see text). See Figure 1 for a graphical representation and characterization of the families with more than one call structure/rate (Vespertilionidae and Mormoopidae).

[illegible]

In addition, we used 345 species for which we have data on both FME and forearm length (FA) to evaluate the hypothesis of constrained evolution of echolocation and body size. The same 18 scenarios were evaluated for this purpose with the function `OUwie.joint` (see Leslie *et al.* 2014) from the R package `OUwie`, also considering a Brownian motion model with one or multiple evolutionary rates. In this function, the evolutionary rates in each hypothetical classification can be constrained or not to be equal between the two traits, and AICc (sample size corrected Akaike Information Criterion) values are returned for the constrained and unconstrained scenarios, through which the hypothesis of joint evolution can be compared. For consistency, we repeated all the analyses using FA alone.

In all cases, the function `ace` from the R package `ape` 3.1.4 (Paradis *et al.* 2004) was used to reconstruct the maximum likelihood ancestral states in the internal nodes of the tree (Schluter *et al.* 1997), assuming equal transition rates between states. In all models we used log transformed values of FME and FA. AICc values and the corresponding Akaike weights ( $AICc_w$ ; Burnham & Anderson 2002) were used to compare the fit of the different models. Akaike weights were used to compute weighted averages of the phylogenetic mean values of FME and FA. All analyses were performed in R 3.1.2 (R Core Team 2014).

## 2.3 Results

The `mccTree` provides the strongest support to the four-rate model H13 ( $AIC_w = 0.54$ ; Figure 2; fifth circle from outward in Figure 1), which assigns most vespertilionids, Craseonycteridae and Rhinopomatidae with the same rate as SBM bats. This model also allocates the families Noctilionidae, Thyropteridae and Mormoopidae – including *P. parnellii* – with the same rate as all other Noctilionoidea, SBM. However, the Akaike weights do not unambiguously support it as the best hypothesis (Table 2; see Burnham & Anderson 2002). The four-rate model that assigns all vespertilionids the SBM rate (H12) appears as second best

( $AICc_w = 0.28$ ) and the model with Craseonycteridae and Rhinopomatidae as NM appears in third (H11,  $AICc_w = 0.06$ ). The original six-rate model (H1), as well as the simpler two-rate model (H17), shows considerably lower support.

H13

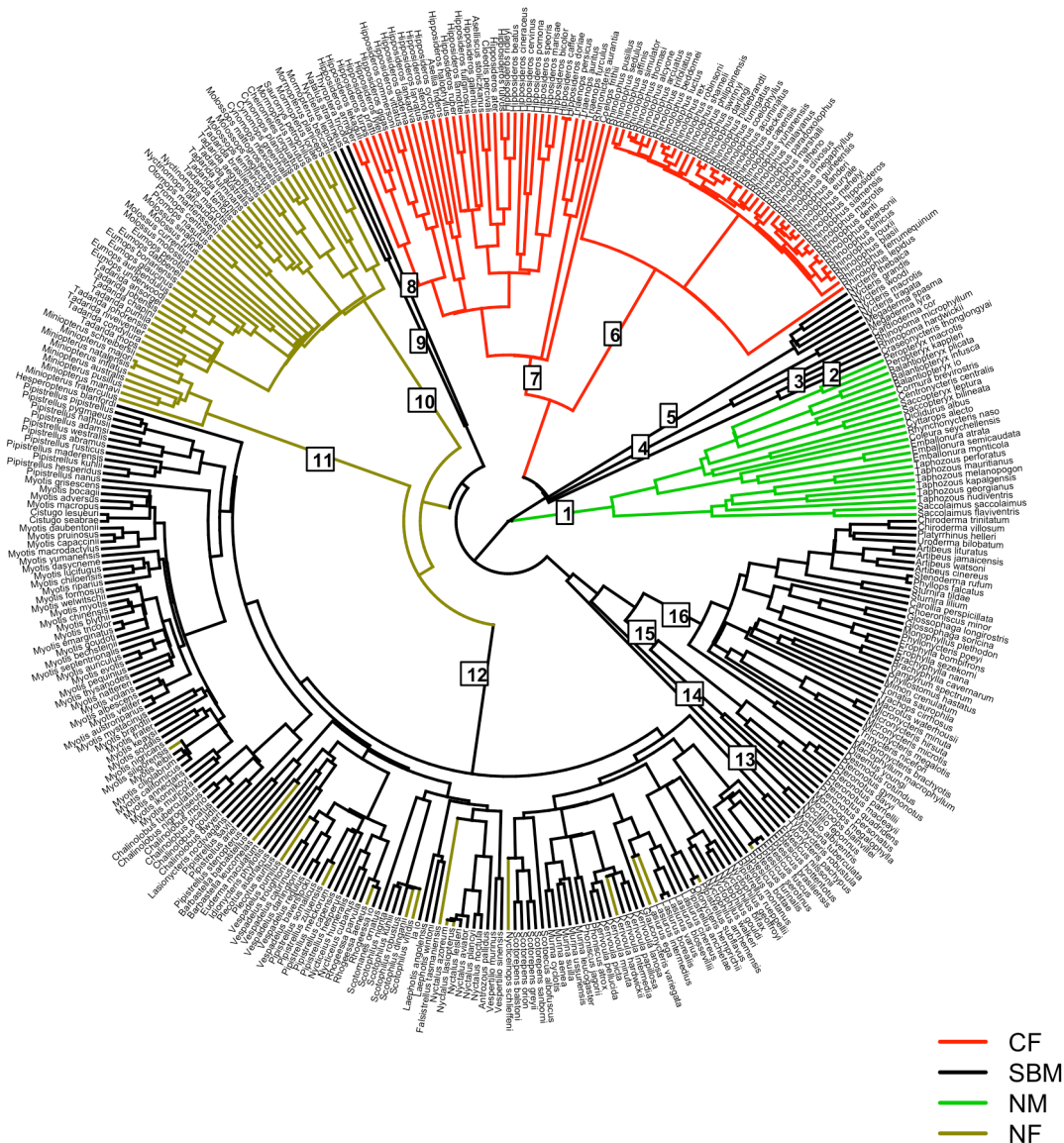


Figure 2: Representation of the hypothesis of differential rates of frequency of maximum energy evolution with greater AICc support, H13. See Figure 1 caption for the family names corresponding to each number along internal branches.

Table 2: Delta AICc and Akaike weights of the 18 models used to evaluate heterogeneity in rates of frequency of maximum energy alone (FME, N = 372 species) and frequency of maximum energy plus forearm length (FME + FA, N = 345), with variable rates between characters (unconstrained) or a common rate between characters (constrained).  $\Delta_{\text{joint}}$  is the AICc of the constrained minus the AICc of the unconstrained models. Models are ordered according to Figure 1, except for the single rate model, BM1, that is not shown in the figure.

Model	Rates	FME		FME + FA unconstrained		FME + FA constrained		$\Delta_{\text{joint}}$
		$\Delta\text{AICc}$	$\text{AICc}_w$	$\Delta\text{AICc}$	$\text{AICc}_w$	$\Delta\text{AICc}$	$\text{AICc}_w$	
<b>BM1</b>	1	198.42	0	290.22	0	325.69	0	86.26
<b>H1</b>	6	7.28	0.014	23.74	0	18.91	0	45.96
<b>H2</b>	6	8.09	0.010	18.05	0	18.47	0	51.21
<b>H3</b>	5	7.61	0.012	21.93	0	18.82	0	47.68
<b>H4</b>	5	6.61	0.020	20.86	0	17.3	0	47.23
<b>H5</b>	5	8.68	0.007	16.57	0	18.76	0	52.98
<b>H6</b>	5	7.44	0.013	15.2	0	16.89	0	52.47
<b>H7</b>	4	8.92	0.006	30.24	0	27.27	0	47.82
<b>H8</b>	4	12.13	0.001	17.96	0	22.79	0	55.61
<b>H9</b>	4	10.73	0.003	16.47	0	20.8	0	55.10
<b>H10</b>	4	5.97	0.027	24.66	0	21.52	0	47.65
<b>H11</b>	4	4.38	0.061	16.31	0	14.25	0.001	48.73
<b>H12</b>	4	1.33	0.279	5.36	0.064	5.66	0.056	51.08
<b>H13</b>	4	<b>0</b>	<b>0.543</b>	<b>0</b>	<b>0.935</b>	<b>0</b>	<b>0.943</b>	50.79
<b>H14</b>	3	12.34	0.001	31.66	0	31.26	0	50.38
<b>H15</b>	3	11.89	0.001	34.42	0	33.78	0	50.14
<b>H16</b>	3	14.04	0	39.75	0	37.69	0	48.73
<b>H17</b>	2	12.29	0.001	42.12	0	38.98	0	47.65

Estimated rates for the preferred model show that CF bats have the highest rate of phenotypic evolution, 5.5% greater than the background SBM (1.061 vs. 1.006, Table 3). In all models, NM species appear to have the lowest rate of evolution, except when vespertilionids are all simplified to this category. In models including the polymorphic category, its rate is similar to that of NM species, but there is little support for the differentiation of Mormoopidae and Noctilionidae from the other Noctilionoidea in the models including all species, and even less support when this difference is evaluated only within the superfamily Noctilionoidea (not shown). All ancestral character reconstructions place SBM as the ancestral state for

the echolocating bats, and the best models indicate that most vespertilionids have frequencies of maximum energy that evolve at the same rate of SBM bats, regarding of the ancestral state of Vespertilionoidea being reconstructed as NF. Nevertheless, in the best model, vespertilionids that emit narrowband calls appear to evolve at the same rate as the NF bats in the superfamily Vespertilionoidea.

Table 3: Estimated rates for the three models with higher AIC<sub>cw</sub>, and the originals six-rate and two-rate models of differential rates of evolution of frequency of maximum energy. Numbers in parenthesis are the approximate 95% confidence intervals, calculated according to Beaulieu *et al.* (2012). Blank cells in each model represent classes that were combined with the SBM class. Models are ordered according to AIC<sub>cw</sub>.

Model	Rates					
	CF	NM	NF	SBF	SBM	P
<b>H13</b>	1.061 (1.041-1.080)	1.002 (1.001 - 1.003)	1.010 (1.006 - 1.014)		1.006 (1.005 - 1.008)	
<b>H12</b>	1.061 (1.041-1.080)	1.003 (1.001 - 1.003)	1.005 (1.003 - 1.008)		1.008 (1.006 - 1.009)	
<b>H11</b>	1.061 (1.041-1.080)	1.003 (1.001 - 1.005)	1.010 (1.006 - 1.014)		1.006 (1.005 - 1.008)	
<b>H1</b>	1.060 (1.041-1.079)	1.003 (1.001 - 1.004)	1.010 (1.006 - 1.014)	1.006 (1.004 - 1.008)	1.007 (1.004 - 1.010)	1.003 (1.000 - 1.006)
<b>H17</b>	1.060 (1.041-1.079)				1.007 (1.006 - 1.008)	

The AICc differences between the constrained and unconstrained models show that FME and FA do not evolve at the same rate in any of the evaluated models (Table 2). Both scenarios, however, clearly indicate the H13 also as the best model, with Akaike weights greater than 0.9. As in the case of FME alone, H12 stands as the second best, but in these cases with much lower AIC<sub>cw</sub> (approximately 0.06 in both scenarios). All unconstrained models show that FA has an overall smaller rate of evolution than FME, majorly for CF and SBM bats (Table 4), and in the constrained scenarios, CF shows a decreased estimate when compared to FME alone, while the other rates appear in the confidence interval estimated for FME rates (Tables 3 and 4). Repeating the analyses with FA alone result in the same models being selected,



with rates identical to those estimated in the unconstrained scenario. This result indicates that frequency of maximum energy and body size evolve in tandem, although with different rates.

Table 4: Estimated rates of evolution of frequency of maximum energy (FME) and forearm length (FA), for the two models with higher AIC<sub>cw</sub>, and the originals six-rate and two-rate models. Unconstrained models estimate separate parameters for FME and FA, while constrained models assume a single rate for both characters. Blank cells in each model represent classes that were combined with the SBM class. Models are ordered according to AIC<sub>cw</sub>.

Model	Character	Unconstrained models					
		CF	NM	NF	SBF	SBM	P
<b>H13</b>	FME	1.064	1.002	1.011		1.007	
	FA	1.017	1.001	1.010		1.003	
<b>H12</b>	FME	1.064	1.002	1.006		1.008	
	FA	1.017	1.001	1.002		1.005	
<b>H1</b>	FME	1.063	1.003	1.011	1.006	1.007	1.003
	FA	1.017	1.002	1.009	1.003	1.002	1.003
<b>H17</b>	FME	1.063				1.007	
	FA	1.017				1.004	
		Constrained models					
<b>H13</b>		1.040	1.001	1.010		1.005	
<b>H12</b>		1.040	1.001	1.004		1.006	
<b>H1</b>		1.040	1.002	1.009	1.005	1.005	1.003
<b>H17</b>		1.040				1.005	

The model-averaged phylogenetic mean of FME has a value of 45.32 kHz (SE = 1.23), similar to that estimated by the constrained and unconstrained models (44.69 and 44.76, respectively). Forearm length also has close estimated phylogenetic means between the constrained and unconstrained scenarios, 49.12 and 49.04 mm, respectively.

## 2.4 Discussion

Echolocation call types are associated with the different habitats in which bats forage, as well as their foraging behaviors (Aldridge & Rautenbach 1987, Schnitzler & Kalko 2001, Schnitzler *et al.* 2003, Denzinger & Schnitzler 2013), leading several authors to suggest the convergence of habitat use and echolocation types among distant bat lineages (Eick *et al.* 2005, Jones & Teeling 2006) due to similar ecological pressures on the evolution of the biosonar. However, we found little support for most hypothesized cases of convergent rates of evolution. The best model allocates 20 species of Vespertilionidae with the same rate as Molossidae and Miniopteridae, and all other species in the family with a reversal to the ancestral rate of echolocating bats, SBM. Moreover, the model simplifying all Vespertilionidae to the same rate cannot be disregarded for FME nor FA, leading to the support of just one case of convergence among all bats. Other echolocation parameters, like bandwidth and call duration, are known to have different structures of phylogenetic dependence (Bilski *et al.* – Chapter 1), and thus can be subject to alternate models of phenotypic evolution.

The preferred model, H13, combines all species that use broadband signals into one single rate. Some vespertilionids that concentrate more energy on the fundamental are known to emit calls with the presence of higher harmonics (Obrist 1995, Jones & Teeling 2006, Fenton *et al.* 2012), and, in some conditions, certain species concentrate more energy on higher harmonics (Bates *et al.* 2011, Fenton *et al.* 2012). Furthermore, H13 includes some species that use narrowband calls with multiple harmonics at the same rate as SBM-SBF bats. These groups live and forage in several disparate conditions, from open xeric habitats in Rhinopomatidae (Qumsiyeh & Jones 1986, Schlitter & Qumsiyeh 1996), up to tropical forests in Thyropteridae and Phyllostomidae (Bernard & Fenton 2002). In addition, Phyllostomidae encompass several dietary patterns besides insectivory (Rojas *et al.* 2011, 2012), although most species are known to consume insects detected through echolocation on an opportunistic manner (Rex *et al.* 2010). Consequently, this grouping cannot be explained by similar environmental or dietary patterns. It is

possible that the grouping of the NM callers simply reflect their difference in relation to the other NM species from Emballonuridae, but a model with a separate rate for these few species would probably generate biased estimates (see O'Meara *et al.* 2006, Beaulieu *et al.* 2012).

The same model selected for FME also explains the variation in FA rates of evolution. This is expected based on the coupling of echolocation modes and frequency with body size (Aldridge & Rautenbach 1987, Norberg & Rayner 1987), and the association of call production with wing beating to diminish the high costs of echolocation (Speakman & Racey 1991, Holderied & von Helversen 2003, Voigt & Lewanzik 2012). The frequency of maximum energy is known to have a negative relation with body size, with larger species emitting lower frequency calls (Jones 1999, Jacobs *et al.* 2007, Bilski *et al.* – Chapter 1). In our results, the highest difference between FME and FA rates is found for CF bats. Several Rhinolophidae species deviate from the allometric scaling between body size and echolocation frequency (Jacobs *et al.* 2007), being the frequencies more closely related to snout length and bite force (Jacobs *et al.* 2014). Moreover, some species in this family are known to adopt a perch-hunting strategy, diminishing their energy requirements (Voigt *et al.* 2010), and perhaps releasing them from the coupling between call production and wing beating.

The finding of a smaller rate of phenotypic evolution in broadband callers and accelerated rates in the more derived echolocation modes, highly adapted to prey detection, is consistent with the view that echolocation evolved first as a spatial orientation mechanism and further switched to prey detection (Schnitzler *et al.* 2003). In addition to facilitating navigation in close space (Denzinger & Schnitzler 2013), broadband signals allow the discrimination of prey items at close distances from the background (Siemers & Schnitzler 2004, Schmieder *et al.* 2012), although there are few known broadband callers capable of finding motionless preys on narrow space environments relying just on echolocation (Geipel *et al.* 2013, Denzinger & Schnitzler 2013. See also Arlettaz *et al.* 2001). Narrowband callers, on the other hand, locate and capture insects in open habitats only using long range, high intensity echolocation (Siemers *et al.* 2001, Schnitzler *et al.* 2003, Jung *et al.*

2014), whereas the highly specialized HDC species use frequency alterations and Doppler shift compensation to separate echoes from background and fluttering insects in narrow space (Fenton *et al.* 1995, 2012). This is not to say that broadband callers are incapable of tracking prey only through echolocation. Species that occupy more dense habitats are known to be capable of assess prey on open space, often changing the echolocation mode and intensity (Kalko & Schnitzler 1993, Jensen & Miller 1999, Brinkløv *et al.* 2010, Hackett *et al.* 2014); but the converse is not true (Fenton 1990, but see Siemers *et al.* 2001), particularly due to the difficulty of open space species in flying in narrow space (Voigt & Holderied 2011).

Trees resolved through the birth-death method of Kuhn *et al.* (2011) tend to pull the species appearance closer to the present (Figure 3; Kuhn *et al.* 2011). This can lead to biased high rates in one group if it has much shorter branches than the other groups with which it is being compared (Thomas *et al.* 2009). Rhinolophidae has notably smaller branches than the rest of the tree, and is thus probably responsible for the higher rate of FME evolution in HDC bats. However, this group shows several cases of partitioning of the acoustical niche space, with low overlapping of maximum energy frequencies among coexisting species (Heller & von Helversen 1989; Kingston *et al.* 2000) and cases of displacement in limited environments (Russo *et al.* 2007). Therefore, this high rate in HDC bats can be reflecting rapid shifts in echolocation frequency caused by niche partitioning (Heller & von Helversen 1989, Moen & Wiens 2009), or a case of cladogenetic evolution (Pennell *et al.* 2014b).

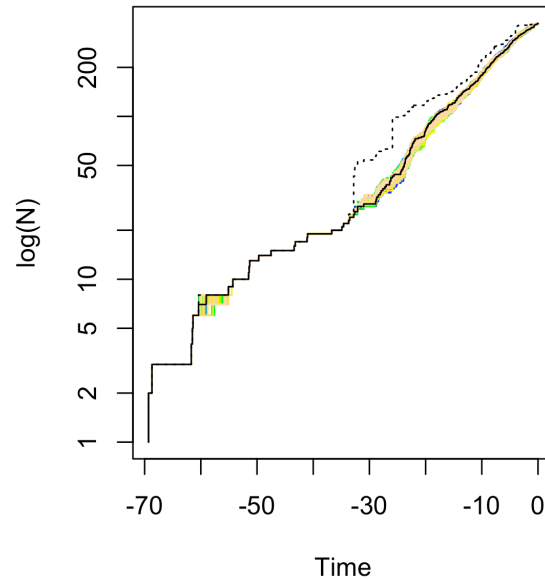


Figure 3: Lineage through time plots for different tree resolutions. Dotted line is the original supertree of Fritz *et al.* (2009); colored lines are 100 polytomy resolutions from Kuhn *et al.* (2011); and the solid black line is the reconstructed maximum clade credibility tree.

The placement of Emballonuridae on the supertree used herein can artificially decrease the rate of evolution in NM compared to SBM. Some molecular phylogenies have put Emballonuridae and Nycteridae (superfamily Emballonuroidea) as sister group of Noctilionoidea and Vespertilionoidea (Eick *et al.* 2005, Teeling *et al.* 2005), with divergence dates around 55 mya, approximately 10 my later than the divergence of Emballonuridae from the other groups in Fritz's *et al.* supertree (although the entire order's dating is shifted towards the present. See also Meredith *et al.* 2011). Rate estimates are proportional to the time of divergence between lineages (Freckleton *et al.* 2002), so the exact placement of a clade in the phylogeny does not affect the calculations, but wrong divergence times often does. By correcting the divergence dates between Emballonuroidea and their sister group, an increase in the rate of evolution for NM can lead it to be in the same range of SBM bats, or even approximate it to the rate of the other species that use narrowband frequencies, but concentrated in the fundamental harmonic (NF). Both scenarios offer interesting interpretations about the rates of evolution in LDC bats:

if NM turns out to be equal to SBM, the only shift in rate from the background SBM would be associated with specializations for long range detection in open space. On the other hand, if NM turns to be equal to NF, the production of a broad frequency spectrum would limit the divergence in FME, irrespective of the number of harmonics present.

A number of other classifications of echolocation types and/or foraging guilds have already been proposed (e.g. Aldridge & Rautenbach 1987, Schnitzler & Kalko 2001, Schnitzler *et al.* 2003, Denzinger & Schnitzler 2013). While some of those have been incorporated and evaluated in our study (H16 is close to Schnitzler's *et al.* 2003), other recent, more complex classifications like Denzinger & Schnitzler's (2013) require a more detailed species level description of habitat use and echolocation characterization. Improving the level of detail in the classification of echolocation types, as well as complete species level phylogenies, can lead to results different from those found herein. However, besides thorough species level characterization, methods capable of confidently pointing rate shifts in small clades have also to be devised (O'Meara *et al.* 2006, Beaulieu *et al.* 2012). We must stress out that our work does not disregard the convergence of echolocation types among distantly related groups (Jones & Teeling 2006, Jones & Holderied 2007), but only points that, in most cases, rates of maximum energy frequency and forearm length evolution are not convergent among groups, still following the rate of phenotypic diversification found in the clades to which they pertain.

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## 2.6 Supplementary material

Table S1: Number of species per family included in the dataset, and the respective number of species described for each family, based on Wilson & Reeder 2005. Note that we follow Miller-Butterworth *et al.* 2007 in recognizing Miniopteridae as a distinct family.

<b>Family</b>	<b>N dataset</b>	<b>Number of species</b>
Craseonycteridae	1	1
Emballonuridae	24	52
Furipteridae	0	2
Hipposideridae	38	85
Megadermatidae	3	5
Miniopteridae	8	24
Molossidae	41	100
Mormoopidae	8	9
Mystacinidae	1	2
Myzopodidae	0	1
Natalidae	2	8
Noctilionidae	2	2
Nycteridae	5	16
Phyllostomidae	37	174
Rhinolophidae	43	77
Rhinopomatidae	2	4
Thyropteridae	1	3
Vespertilionidae	156	392

Table S2: Sources of peak echolocation frequency information for each species. FA represents the species with forearm length information. References are numbered according to the supplementary references list.

Species	FA	References
<i>Craseonycteris thonglongyai</i>	FA	53, 143
<i>Balantiopteryx infusca</i>	FA	59
<i>Balantiopteryx io</i>	FA	59
<i>Balantiopteryx plicata</i>	FA	14, 59, 109
<i>Centronycteris centralis</i>		14, 70
<i>Coleura seychellensis</i>	FA	4, 44
<i>Cormura brevirostris</i>	FA	34, 70
<i>Cyttarops alecto</i>	FA	70
<i>Diclidurus albus</i>	FA	70
<i>Emballonura atrata</i>	FA	78
<i>Emballonura monticola</i>	FA	119
<i>Emballonura semicaudata</i>	FA	46
<i>Peropteryx kappleri</i>	FA	70
<i>Peropteryx macrotis</i>	FA	9, 14 89, 126
<i>Rhynchonycteris naso</i>	FA	33, 105, 118
<i>Saccolaimus flaviventris</i>	FA	93
<i>Saccolaimus saccolaimus</i>	FA	119
<i>Saccopteryx bilineata</i>	FA	9, 70, 88, 89, 105, 118
<i>Saccopteryx leptura</i>	FA	9, 70, 118
<i>Taphozous georgianus</i>	FA	94
<i>Taphozous kapalgensis</i>	FA	94
<i>Taphozous mauritanus</i>	FA	28, 98, 132, 144
<i>Taphozous melanopogon</i>	FA	119, 149
<i>Taphozous nudiventris</i>	FA	8
<i>Taphozous perforatus</i>	FA	7, 8, 34
<i>Asellia tridens</i>	FA	7, 66
<i>Aselliscus stoliczkanus</i>	FA	81, 151
<i>Cloeotis percivali</i>	FA	95, 98, 132, 144
<i>Coelops frithii</i>	FA	151
<i>Hipposideros armiger</i>	FA	56, 117, 151, 155
<i>Hipposideros ater</i>	FA	38
<i>Hipposideros beatus</i>	FA	96
<i>Hipposideros bicolor</i>	FA	23, 56, 76
<i>Hipposideros caffer</i>	FA	95, 98, 132, 144
<i>Hipposideros cervinus</i>	FA	76
<i>Hipposideros cineraceus</i>	FA	22, 56, 76, 117
<i>Hipposideros commersoni</i>	FA	78
<i>Hipposideros cyclops</i>	FA	20
<i>Hipposideros diadema</i>	FA	47, 56, 93
<i>Hipposideros doriae</i>	FA	76
<i>Hipposideros fuliginosus</i>	FA	27
<i>Hipposideros fulvus</i>	FA	76
<i>Hipposideros galeritus</i>	FA	56, 117
<i>Hipposideros gigas</i>	FA	96
<i>Hipposideros halophyllus</i>	FA	22, 56
<i>Hipposideros lamottei</i>	FA	96
<i>Hipposideros lankadiva</i>	FA	108
<i>Hipposideros larvatus</i>	FA	56, 117, 140, 147, 155
<i>Hipposideros lekaguli</i>	FA	56

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<i>Hipposideros lylei</i>	FA	140
<i>Hipposideros marisae</i>	FA	96
<i>Hipposideros pomona</i>	FA	23, 117, 140
<i>Hipposideros pratti</i>	FA	151
<i>Hipposideros ridleyi</i>	FA	49, 76
<i>Hipposideros ruber</i>	FA	29, 48, 98
<i>Hipposideros speoris</i>	FA	115
<i>Hipposideros stenotis</i>	FA	93
<i>Hipposideros turpis</i>	FA	56
<i>Hipposideros vittatus</i>		98, 132
<i>Rhinonictes aurantia</i>	FA	2
<i>Triaenops auritus</i>		78
<i>Triaenops furculus</i>	FA	78
<i>Triaenops persicus</i>	FA	98
<i>Cardioderma cor</i>	FA	19
<i>Megaderma lyra</i>	FA	117, 122
<i>Megaderma spasma</i>	FA	117
<i>Miniopterus australis</i>	FA	38
<i>Miniopterus fraterculus</i>	FA	92, 98, 132
<i>Miniopterus inflatus</i>	FA	98
<i>Miniopterus majori</i>	FA	78, 121
<i>Miniopterus manavi</i>	FA	78, 121
<i>Miniopterus natalensis</i>	FA	92, 98, 132
<i>Miniopterus pusillus</i>	FA	117
<i>Miniopterus schreibersii</i>	FA	107, 111, 125, 132
<i>Cheiromeles torquatus</i>	FA	75
<i>Cynomops greenhalli</i>		71
<i>Cynomops mexicanus</i>		14, 90
<i>Cynomops planirostris</i>	FA	71
<i>Eumops auripendulus</i>	FA	71
<i>Eumops bonariensis</i>	FA	71
<i>Eumops dabbenei</i>		71
<i>Eumops glaucinus</i>	FA	71, 101
<i>Eumops perotis</i>	FA	3
<i>Eumops underwoodi</i>	FA	109
<i>Molossops mattogrossensis</i>	FA	71
<i>Molossops neglectus</i>	FA	71
<i>Molossops temminckii</i>	FA	50, 71
<i>Molossus currentium</i>	FA	71
<i>Molossus molossus</i>	FA	14, 71, 106, 118
<i>Molossus rufus</i>	FA	14, 32, 34, 71, 89, 106
<i>Molossus sinaloae</i>	FA	14, 71, 89, 106, 109
<i>Mormopterus beccarii</i>	FA	93
<i>Mormopterus loriae</i>	FA	93
<i>Mormopterus minutus</i>	FA	100
<i>Mormopterus planiceps</i>	FA	39
<i>Nyctinomops laticaudatus</i>	FA	14, 71, 89
<i>Nyctinomops macrotis</i>	FA	3, 9, 71, 101
<i>Otomops martiensseni</i>	FA	30, 132
<i>Promops centralis</i>	FA	71
<i>Promops nasutus</i>	FA	71
<i>Sauromys petrophilus</i>	FA	131, 132
<i>Tadarida aegyptiaca</i>	FA	30, 131, 132, 144
<i>Tadarida ansorgei</i>	FA	98, 144
<i>Tadarida australis</i>	FA	39, 40

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<i>Tadarida brasiliensis</i>	FA	3, 9, 71, 91, 103, 109, 124
<i>Tadarida chapini</i>	FA	144
<i>Tadarida condylura</i>	FA	31, 98, 132, 144
<i>Tadarida fulminans</i>	FA	28
<i>Tadarida insignis</i>		41
<i>Tadarida jobensis</i>	FA	93
<i>Tadarida johorensis</i>	FA	75
<i>Tadarida mops</i>	FA	75
<i>Tadarida niveiventer</i>	FA	132
<i>Tadarida pumila</i>	FA	30, 31, 98, 132, 144
<i>Tadarida teniotis</i>	FA	7, 8, 107, 111, 125
<i>Mormoops blainvillei</i>	FA	65, 85
<i>Mormoops megalophylla</i>	FA	14, 89, 109, 136
<i>Pteronotus davyi</i>	FA	9, 14, 65, 89, 105, 109, 126, 136
<i>Pteronotus gymnonotus</i>	FA	60
<i>Pteronotus macleayii</i>	FA	85
<i>Pteronotus parnellii</i>	FA	14, 65, 85, 89, 105, 109, 126, 136
<i>Pteronotus personatus</i>	FA	14, 89, 90, 105, 109, 136
<i>Pteronotus quadridens</i>	FA	65, 85
<i>Mystacina tuberculata</i>	FA	68, 112, 113
<i>Natalus stramineus</i>	FA	65, 126
<i>Nyctiellus lepidus</i>	FA	103
<i>Noctilio albiventris</i>	FA	55, 73
<i>Noctilio leporinus</i>	FA	14, 106, 130
<i>Nycteris grandis</i>	FA	52, 144
<i>Nycteris macrotis</i>	FA	29, 132
<i>Nycteris thebaica</i>	FA	98, 131, 132, 144
<i>Nycteris tragata</i>	FA	119
<i>Nycteris woodi</i>	FA	144
<i>Artibeus cinereus</i>	FA	118
<i>Artibeus jamaicensis</i>	FA	65, 91, 99, 118
<i>Artibeus lituratus</i>	FA	118
<i>Artibeus watsoni</i>	FA	45, 79
<i>Brachyphylla cavernarum</i>	FA	65
<i>Brachyphylla nana</i>	FA	86
<i>Carollia perspicillata</i>	FA	11, 118, 148
<i>Chiroderma trinitatum</i>	FA	118
<i>Chiroderma villosus</i>	FA	118
<i>Choeroniscus minor</i>	FA	118
<i>Desmodus rotundus</i>	FA	118
<i>Diaemus youngi</i>	FA	17
<i>Erophylla bombifrons</i>	FA	65
<i>Erophylla sezekorni</i>	FA	103
<i>Glossophaga longirostris</i>	FA	65
<i>Glossophaga soricina</i>	FA	118
<i>Lampronnycteris brachyotis</i>	FA	118
<i>Macrophyllum macrophyllum</i>	FA	12, 13, 150
<i>Macrotus waterhousii</i>	FA	103
<i>Micronycteris hirsuta</i>	FA	118
<i>Micronycteris megalotis</i>	FA	35, 118
<i>Micronycteris microtis</i>		43
<i>Micronycteris minuta</i>	FA	118
<i>Mimon crenulatum</i>	FA	118
<i>Monophyllus plethodon</i>	FA	65, 91
<i>Phyllonycteris poeyi</i>	FA	99

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<i>Phyllops falcatus</i>	FA	87, 99
<i>Phyllostomus hastatus</i>	FA	72, 118
<i>Platyrrhinus helleri</i>	FA	118
<i>Stenoderma rufum</i>	FA	65
<i>Sturnira lilium</i>	FA	65
<i>Sturnira tildae</i>	FA	118
<i>Tonatia saurophila</i>	FA	118
<i>Trachops cirrhosus</i>	FA	6, 47, 142
<i>Trinycteris nicefori</i>	FA	118
<i>Uroderma bilobatum</i>	FA	118
<i>Vampyrum spectrum</i>	FA	118
<i>Rhinolophus acuminatus</i>	FA	56, 76
<i>Rhinolophus affinis</i>	FA	56, 76, 117
<i>Rhinolophus alcyone</i>	FA	27
<i>Rhinolophus arcuatus</i>	FA	133
<i>Rhinolophus beddomei</i>	FA	138
<i>Rhinolophus blasii</i>	FA	8, 62, 98, 111, 132
<i>Rhinolophus capensis</i>	FA	62, 132
<i>Rhinolophus clivosus</i>	FA	7, 8, 62, 98, 131, 132
<i>Rhinolophus coelophyllus</i>	FA	56, 61, 76
<i>Rhinolophus darlingi</i>	FA	62, 98, 132
<i>Rhinolophus deckenii</i>	FA	97, 98
<i>Rhinolophus denti</i>	FA	62, 132
<i>Rhinolophus euryale</i>	FA	111, 125, 127
<i>Rhinolophus ferrumequinum</i>	FA	8, 36, 41, 83, 107, 111, 114, 123, 125, 141
<i>Rhinolophus fumigatus</i>	FA	62, 97, 132
<i>Rhinolophus guineensis</i>	FA	27
<i>Rhinolophus hildebrandti</i>	FA	62, 76, 98, 132
<i>Rhinolophus hipposideros</i>	FA	7, 76, 107, 111, 114, 123, 125
<i>Rhinolophus landeri</i>	FA	27, 29, 62, 76, 97, 132
<i>Rhinolophus lepidus</i>	FA	56, 76, 119
<i>Rhinolophus luctus</i>	FA	56, 76, 119, 151
<i>Rhinolophus macrotis</i>	FA	76
<i>Rhinolophus malayanus</i>	FA	56, 76, 117, 137
<i>Rhinolophus marshalli</i>	FA	151
<i>Rhinolophus megaphyllus</i>	FA	38
<i>Rhinolophus mehelyi</i>	FA	7, 111, 127
<i>Rhinolophus paradoxolophus</i>	FA	25, 151
<i>Rhinolophus pearsonii</i>	FA	56, 76
<i>Rhinolophus philippinensis</i>	FA	77
<i>Rhinolophus pusillus</i>	FA	56, 76, 117, 151
<i>Rhinolophus rex</i>	FA	151
<i>Rhinolophus robinsoni</i>	FA	56
<i>Rhinolophus rouxii</i>	FA	104
<i>Rhinolophus sedulus</i>	FA	76
<i>Rhinolophus shameli</i>	FA	56, 61, 117
<i>Rhinolophus siamensis</i>		151
<i>Rhinolophus simulator</i>	FA	62, 98, 132
<i>Rhinolophus sinicus</i>	FA	151
<i>Rhinolophus steno</i>	FA	56, 76, 137, 151
<i>Rhinolophus swinnyi</i>	FA	62, 132
<i>Rhinolophus thomasi</i>		57
<i>Rhinolophus trifoliatus</i>	FA	56, 76, 119
<i>Rhinolophus yunanensis</i>	FA	56, 151
<i>Rhinopoma hardwickii</i>	FA	34

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<i>Rhinopoma microphyllum</i>	FA	8, 21
<i>Thyroptera tricolor</i>	FA	33
<i>Antrozous pallidus</i>	FA	28
<i>Barbastella barbastellus</i>	FA	107, 114, 123, 125
<i>Barbastella leucomelas</i>	FA	8
<i>Chalinolobus dwyeri</i>	FA	116
<i>Chalinolobus gouldii</i>	FA	39, 40
<i>Chalinolobus morio</i>	FA	39
<i>Chalinolobus nigrogriseus</i>	FA	93
<i>Chalinolobus picatus</i>	FA	116
<i>Chalinolobus tuberculatus</i>	FA	112, 113
<i>Cistugo lesueuri</i>	FA	131, 132
<i>Cistugo seabrae</i>	FA	132
<i>Eptesicus bottae</i>	FA	7, 8, 54
<i>Eptesicus brasiliensis</i>	FA	118
<i>Eptesicus furinalis</i>	FA	89, 106, 126
<i>Eptesicus fuscus</i>	FA	3, 14, 24, 34, 99, 102
<i>Eptesicus hottentotus</i>	FA	131, 132
<i>Eptesicus nilssonii</i>	FA	36, 107
<i>Eptesicus serotinus</i>	FA	107, 111, 114, 123, 125
<i>Euderma maculatum</i>	FA	37, 80
<i>Falsistrellus tasmaniensis</i>	FA	51, 116
<i>Glauconycteris variegata</i>	FA	132
<i>Hesperoptenus blanfordi</i>	FA	75, 117
<i>Histiotus montanus</i>	FA	124
<i>Ia io</i>	FA	146
<i>Idionycteris phyllotis</i>	FA	135
<i>Kerivoula hardwickii</i>	FA	117
<i>Kerivoula intermedia</i>	FA	74, 129
<i>Kerivoula lanosa</i>	FA	98
<i>Kerivoula minuta</i>	FA	74
<i>Kerivoula papillosa</i>	FA	74, 129
<i>Kerivoula pellucida</i>	FA	74, 129
<i>Kerivoula picta</i>	FA	139
<i>Laephotis angolensis</i>	FA	28
<i>Laephotis wintoni</i>	FA	64, 132
<i>Lasionycteris noctivagans</i>	FA	5, 24, 106
<i>Lasiurus blossevillei</i>	FA	14, 69
<i>Lasiurus borealis</i>	FA	18, 24, 102, 103
<i>Lasiurus cinereus</i>	FA	5, 24, 40, 106
<i>Lasiurus ega</i>	FA	69, 89, 106, 126
<i>Lasiurus intermedius</i>	FA	14, 89, 126
<i>Lasiurus varius</i>		124
<i>Murina aenea</i>	FA	74
<i>Murina cyclotis</i>	FA	74, 129
<i>Murina leucogaster</i>	FA	36, 41, 83, 141
<i>Murina suilla</i>	FA	74, 129
<i>Murina ussuriensis</i>	FA	36, 41
<i>Myotis adversus</i>	FA	40, 119, 134
<i>Myotis albescens</i>	FA	10
<i>Myotis annectans</i>		117
<i>Myotis auriculus</i>	FA	134
<i>Myotis austroriparius</i>	FA	18
<i>Myotis bechsteinii</i>	FA	107, 111, 114, 123, 134
<i>Myotis blythii</i>	FA	107, 111, 125

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<i>Myotis bocagii</i>	FA	98, 132
<i>Myotis brandtii</i>	FA	107, 114, 123, 128, 134
<i>Myotis californicus</i>	FA	42, 106, 134
<i>Myotis capaccinii</i>	FA	107, 111, 125
<i>Myotis chiloensis</i>	FA	110, 124
<i>Myotis chinensis</i>	FA	83
<i>Myotis ciliolabrum</i>	FA	42, 106
<i>Myotis dasycneme</i>	FA	15
<i>Myotis daubentonii</i>	FA	107, 111, 114, 123, 125, 128, 141
<i>Myotis emarginatus</i>	FA	107, 111, 125, 134
<i>Myotis evotis</i>	FA	47
<i>Myotis formosus</i>	FA	141
<i>Myotis frater</i>	FA	154
<i>Myotis goudoti</i>	FA	78
<i>Myotis grisescens</i>	FA	18, 102
<i>Myotis ikonnikovi</i>	FA	36, 141
<i>Myotis keaysi</i>	FA	89, 126
<i>Myotis leibii</i>	FA	18, 102, 134
<i>Myotis lucifugus</i>	FA	18, 24, 29, 102, 134
<i>Myotis macrodactylus</i>	FA	36, 41
<i>Myotis macropus</i>		93
<i>Myotis muricola</i>	FA	119
<i>Myotis myotis</i>	FA	107, 111, 125
<i>Myotis mystacinus</i>	FA	107, 111, 114, 123, 125, 134
<i>Myotis nattereri</i>	FA	8, 41, 107, 114, 123, 125, 134
<i>Myotis nigricans</i>	FA	69, 118, 134
<i>Myotis pequinius</i>	FA	67
<i>Myotis pruinus</i>	FA	41
<i>Myotis riparius</i>	FA	33
<i>Myotis septentrionalis</i>	FA	18, 24, 102
<i>Myotis siligorensis</i>	FA	143
<i>Myotis sodalis</i>	FA	18, 102
<i>Myotis thysanodes</i>	FA	134
<i>Myotis tricolor</i>	FA	98, 131, 132, 144
<i>Myotis velifer</i>	FA	109
<i>Myotis volans</i>	FA	134
<i>Myotis welwitschii</i>	FA	132
<i>Myotis yumanensis</i>	FA	106, 109
<i>Nyctalus aviator</i>	FA	36, 41
<i>Nyctalus azoreum</i>	FA	120
<i>Nyctalus lasiopterus</i>	FA	26, 58
<i>Nyctalus leisleri</i>	FA	16, 107, 111, 114, 120, 123, 125, 145
<i>Nyctalus noctula</i>	FA	26, 107, 111, 114, 123, 125
<i>Nyctalus plancyi</i>		156
<i>Nycticeinops schlieffeni</i>	FA	31, 98, 132
<i>Nycticeius cubanus</i>		99
<i>Nycticeius humeralis</i>	FA	18, 102
<i>Nyctophilus arnhemensis</i>	FA	93
<i>Nyctophilus bifax</i>	FA	93, 116
<i>Nyctophilus geoffroyi</i>	FA	39, 40
<i>Nyctophilus gouldi</i>	FA	39
<i>Nyctophilus walkeri</i>	FA	93
<i>Otonycteris hemprichii</i>	FA	7, 8
<i>Phoniscus atrox</i>	FA	74, 129
<i>Phoniscus jagorii</i>	FA	74, 129

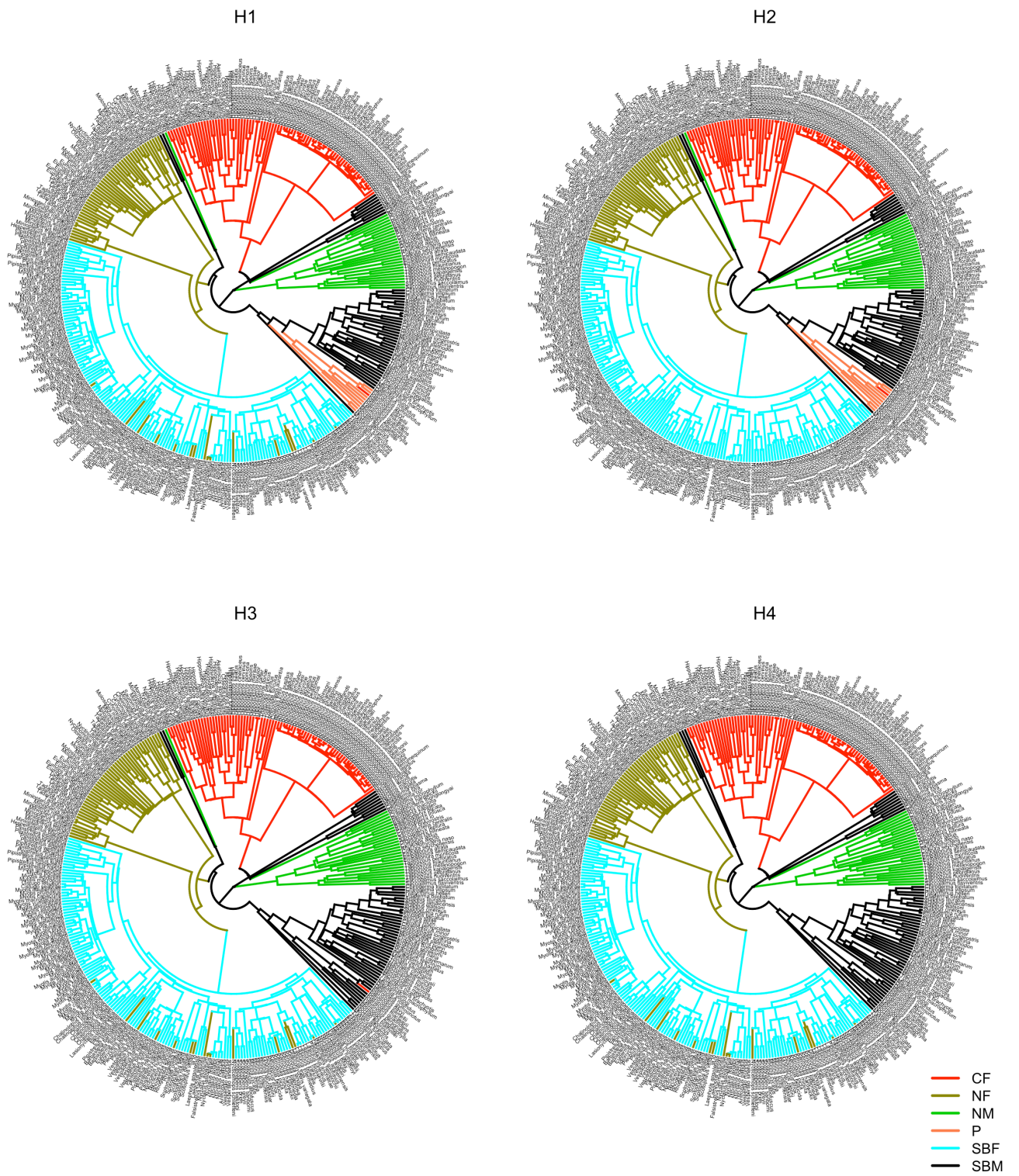
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<i>Pipistrellus abramus</i>	FA	41, 82
<i>Pipistrellus adamsi</i>		93
<i>Pipistrellus anchietae</i>		132
<i>Pipistrellus ariel</i>	FA	7, 8
<i>Pipistrellus capensis</i>		31, 98, 131, 132
<i>Pipistrellus hesperidus</i>		98, 132
<i>Pipistrellus hesperus</i>	FA	47
<i>Pipistrellus kuhlii</i>	FA	8, 107, 111, 125
<i>Pipistrellus maderensis</i>	FA	120, 145
<i>Pipistrellus melckorum</i>		144
<i>Pipistrellus nanus</i>	FA	29, 31, 144
<i>Pipistrellus nathusii</i>	FA	107, 111
<i>Pipistrellus pipistrellus</i>	FA	8, 107, 111, 114, 123, 125, 128
<i>Pipistrellus pygmaeus</i>		207, 111, 114, 123, 125
<i>Pipistrellus rueppellii</i>	FA	28
<i>Pipistrellus rusticus</i>	FA	31, 132, 144
<i>Pipistrellus savii</i>	FA	107, 111, 125
<i>Pipistrellus somalicus</i>		78
<i>Pipistrellus stenopterus</i>	FA	75
<i>Pipistrellus subflavus</i>	FA	18, 24, 84, 102
<i>Pipistrellus westralis</i>		93
<i>Pipistrellus zuluensis</i>		98, 132
<i>Plecotus auritus</i>	FA	107, 123, 125
<i>Plecotus austriacus</i>	FA	107, 111, 120, 125, 145
<i>Rhogeessa aeneus</i>	FA	89, 126
<i>Rhogeessa io</i>	FA	118
<i>Rhogeessa parvula</i>	FA	109
<i>Scotoecus albobfuscus</i>	FA	132
<i>Scotomanes ornatus</i>	FA	1
<i>Scotophilus dinganii</i>	FA	63, 98, 132
<i>Scotophilus kuhlii</i>	FA	119
<i>Scotophilus nigrita</i>	FA	28
<i>Scotophilus robustus</i>	FA	78
<i>Scotophilus viridis</i>	FA	31, 98
<i>Scotorepens balstoni</i>	FA	116
<i>Scotorepens greyii</i>	FA	93, 116
<i>Scotorepens orion</i>		116
<i>Scotorepens sanborni</i>	FA	93
<i>Tylonycteris pachypus</i>	FA	117, 152, 153
<i>Tylonycteris robustula</i>	FA	119, 152, 153
<i>Vespadelus baverstocki</i>	FA	116
<i>Vespadelus caurinus</i>		93
<i>Vespadelus darlingtoni</i>	FA	51, 116
<i>Vespadelus pumilus</i>	FA	40
<i>Vespadelus regulus</i>	FA	39
<i>Vespadelus troughtoni</i>		116
<i>Vespertilio murinus</i>	FA	107
<i>Vespertilio sinensis</i>	FA	36, 41

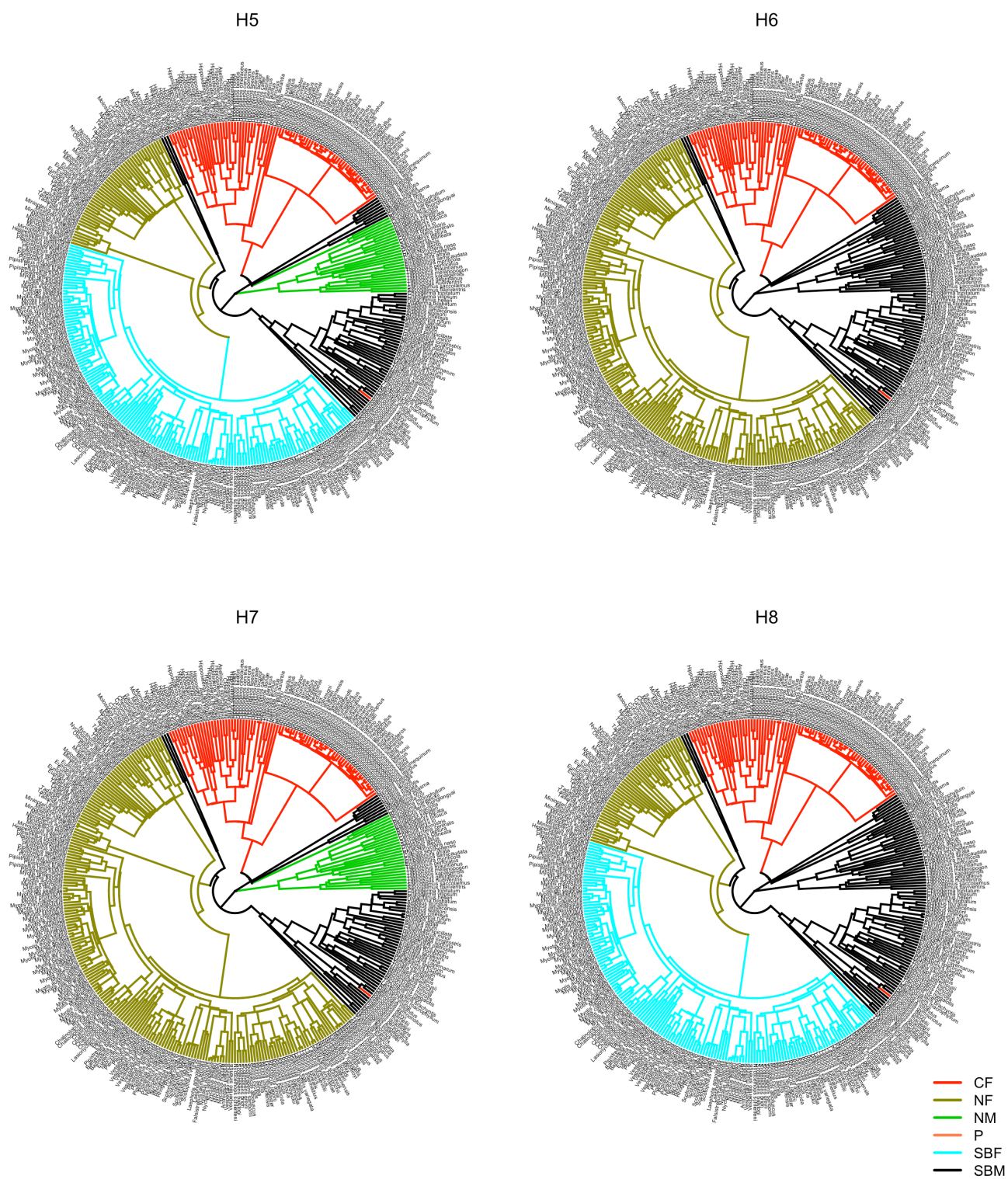
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Supporting Figure S1: Evaluated hypotheses of differential rates of peak echolocation frequency and forearm length evolution.

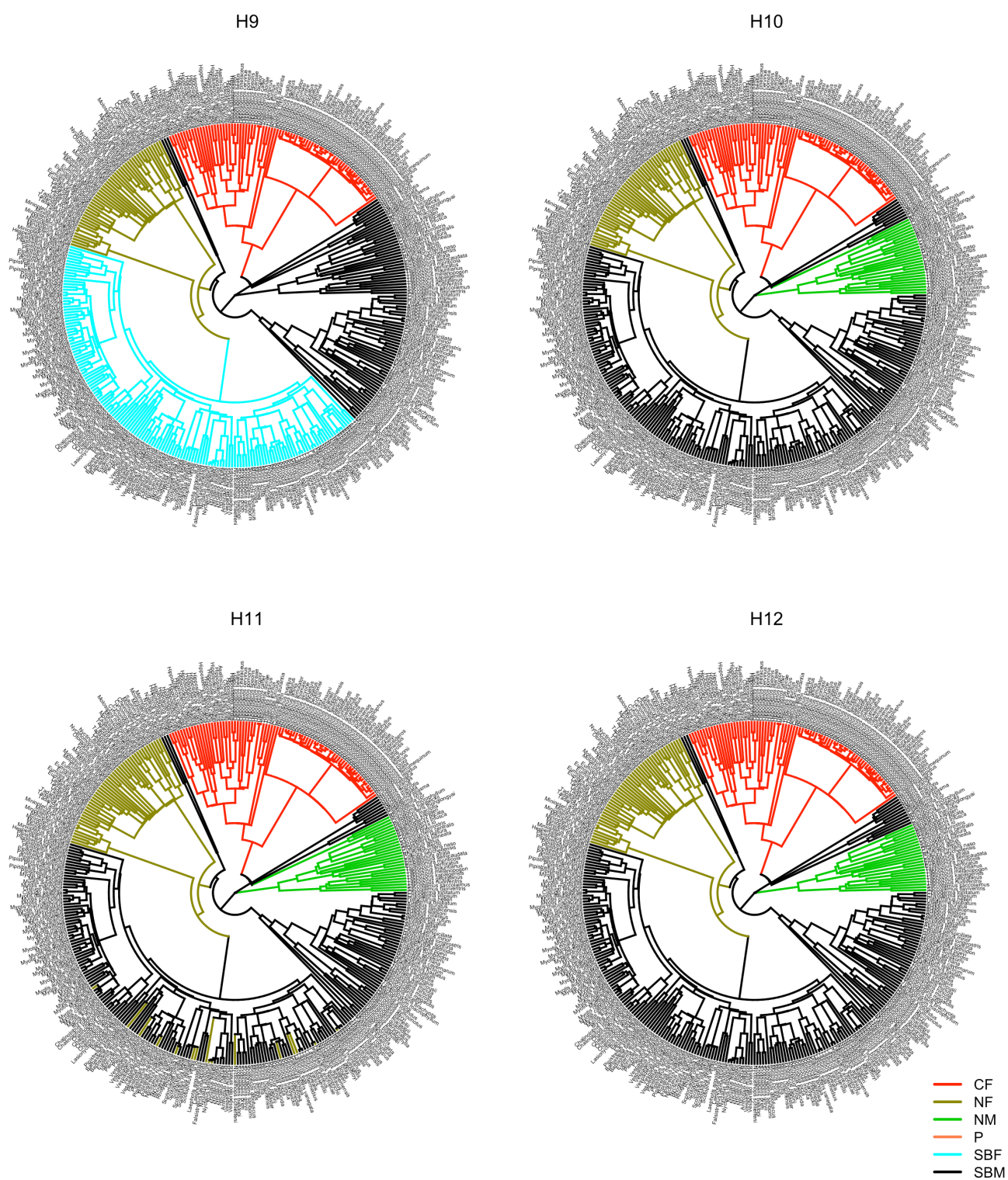




Supporting Figure S1 (continued)

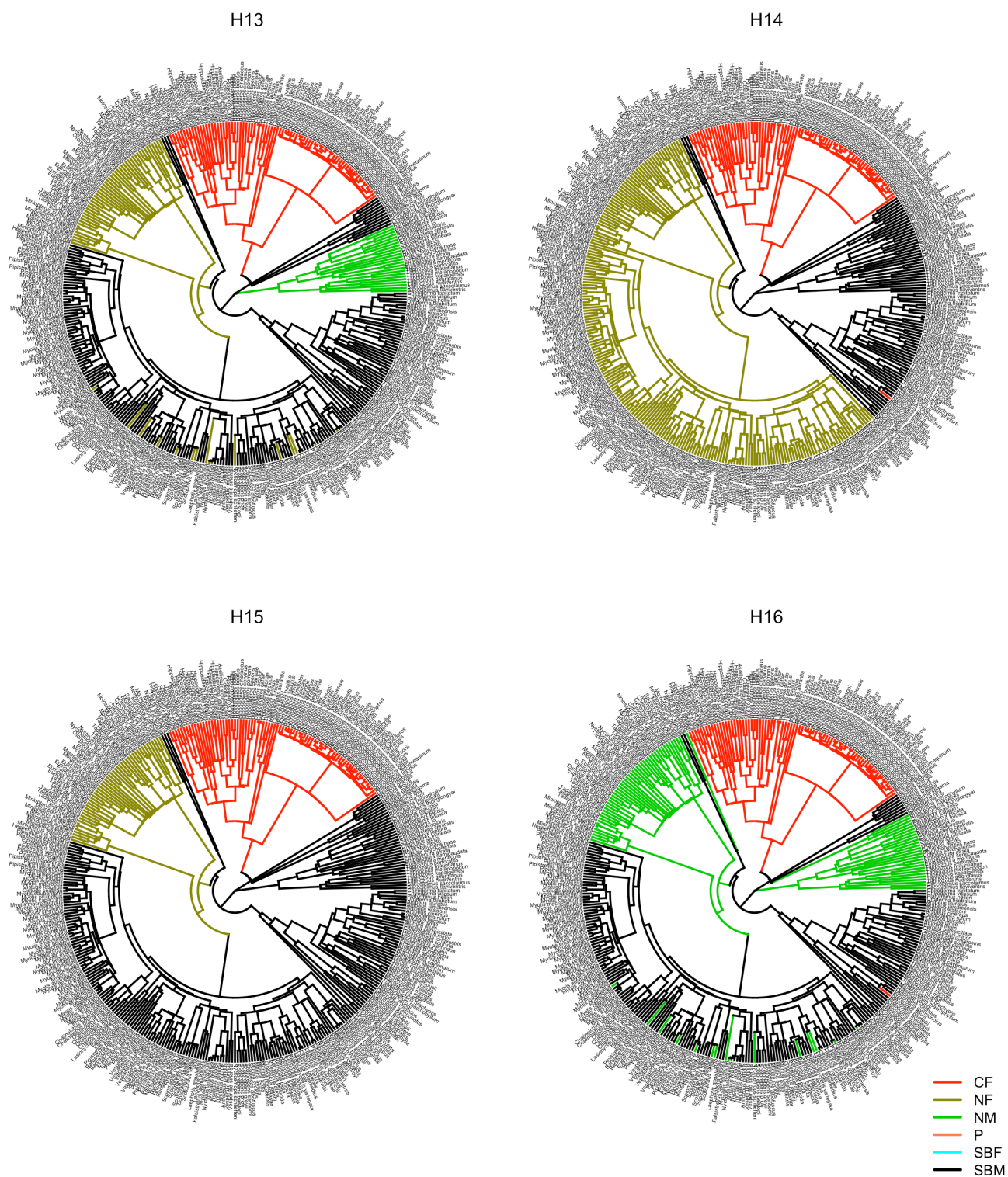


Supporting Figure S1 (continued)





Supporting Figure S1 (continued)



— HDC  
— LDC

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## **CAPÍTULO 3**

### **SOUND ATTENUATION AND THE GLOBAL RICHNESS GRADIENT OF ECHOLOCATING BATS**

### 3.1 Introduction

The geographical patterns of species richness have been extensively studied in the last decades (reviewed in Rosenzweig 1995, Willig *et al.* 2003, Field *et al.* 2009). Most studies relate the richness gradient to current or historical climatic variables (e.g. Hawkins *et al.* 2007, Davies *et al.* 2011) and/or to water and productivity (e.g. Mittelbach *et al.* 2001, Hawkins *et al.* 2003, Whittaker *et al.* 2007). Mammals show a pronounced climate-richness relationship (Buckley *et al.* 2010), primarily caused by strong tropical niche conservatism in bats (Buckley *et al.* 2010, Stevens 2011). However, some necessary predictions of this tropical niche conservatism have been put into question for some groups of New World bats (Pereira & Palmeirim 2013, Arita *et al.* 2014). Although climate and energy emerge as the correlates of species richness, several large-scale patterns are the outcome of mechanisms occurring at smaller scales (Wiens & Donoghue 2004, Tello & Stevens 2012), but processes linking these scales have proven elusive (Currie *et al.* 2004, Evans *et al.* 2005).

The abilities to fly and echolocate are assumed to be the major basis for the exceptional bat diversity (Simmons 2005, Jones & Teeling 2006). Echolocation is an active process present in all members of at least 18 of the 19 families of bats, and recent findings confirm that echolocation abilities are more widespread within this remaining family than previously thought (Gould 1988, Boonman *et al.* 2014). Navigation is the most prominent role of echolocation, probably present in all species that echolocate, and several species also use it to detect and approach food items (Griffin *et al.* 1960, Schnitzler & Kalko 2001, Korine & Kalko 2005). To form an auditory scene, bats need to dynamically integrate timing and frequency content from the target as well as several other sources of echoes in the background (Moss & Surlykke 2010, Schmieder *et al.* 2012). As a consequence, similar environments and diets might lead to similar call characteristics among the species that occupy each habitat (Schnitzler & Kalko 2001, Schnitzler *et al.* 2003, Surlykke & Kalko 2008), but in an interplay with constraints imposed by phylogenetic history (Bilski *et al.* – Chapter 1).

Most bat species produce sounds of ultrasonic frequencies (Griffin *et al.* 1960, Davies *et al.* 2013, Fenton 2013). Several studied communities are composed by bats echolocating in the range between 20 and 60 kHz, the frequency range best suited to the detection of small insects (Jones & Holderied 2007), but tropical communities also have species calling below and above those thresholds (Heller & von Helversen 1989, Fenton *et al.* 1998, Jung *et al.* 2007, 2014). Higher frequencies provide better detailing for the bat, but also lose energy more rapidly than low frequencies, which are capable of spreading for long distances (Fenton *et al.* 1998, Holderied & von Helversen 2003). Besides the spreading loss of a sound wave propagating in the open space, high frequencies are severely attenuated through atmospheric absorption (Lawrence & Simmons 1982, Kuttruff 1991, Attenborough 2007, Stilz & Schnitzler 2012). Atmospheric sound attenuation is a non-linear function of frequency, temperature and humidity (Lawrence & Simmons 1982, Attenborough 2007, Stilz & Schnitzler 2012). Its relation with sound frequency is monotonic, increasing for higher frequencies, while the relation with humidity grows until a peak, then falls back (Supplementary Figure S1). Griffin (1971) was the first to note that the range of frequencies used by insectivorous bats are the most severely attenuated in tropical conditions of temperature and humidity. He also noted that the tropics hold a suit of species that emit low frequency calls, which are much less affected by atmospheric attenuation (Griffin 1971).

As the echolocation is a self-communication mechanism, the bat needs to distinguish the echo of its own call from other sounds in the environment (Obrist 1995, Neuweiler 2003, Tressler & Smotherman 2009). Flying in close proximity with conspecifics may elicit the adoption of responses to avoid jamming, through shifts in the timing of calls (Obrist 1995), alteration of call frequency (Surlykke & Moss 2000, Ibáñez *et al.* 2004, Ratcliffe *et al.* 2004, Ulanovsky *et al.* 2004, Gillam *et al.* 2007, Bates *et al.* 2008), or both (Takahashi *et al.* 2014). Jamming avoidance has also been shown among separate species with similar calls (Necknig & Zahn 2011), and the partitioning of the sound space has been proposed as the mechanism responsible for interspecific differences in call frequency in some bat communities (Heller & von Helversen 1989, Russo *et al.* 2007, see also Kingston *et al.* 2000).

Despite being produced to acquire information, echolocation calls also convey information to eavesdroppers (Fenton 2003). It may attract conspecifics to feeding opportunities (Balcombe & Fenton 1988, Gillam 2007, Dechmann *et al.* 2009), and interspecific attraction has also been shown (Dorado-Correa *et al.* 2013). This process has commonly been viewed in a communicative context (Jones & Siemers 2010), but recent findings show that conspecifics may compete for food in an antagonistic manner, with individuals emitting calls to repel (Wright *et al.* 2014) or even disrupt the feeding approaches of its neighbors (Corcoran & Conner 2014).

Bats that use broadband calls have wider room for intra and interspecific spectral overlap, and hence are more likely to experience jamming than species that use narrowband calls (Ulanovsky *et al.* 2004). Moreover, broadband callers do not have ear cells and auditory brain centers sharply tuned to highly specialized frequencies, like those found in high duty cycle species (Vater & Kössl 2004, von Stebut & Schmidt 2004), providing them more room to vocal adaptations. However, spectral and temporal alterations of preferred echolocation characteristics disrupt the scaling of these characteristics with body size and wing beating, and possibly alter the bat's detection abilities (Speakman & Racey 1991, Fenton *et al.* 1998, Jones 1999, Holderied & von Helversen 2003, Voigt & Lewanzik 2012).

Considering that there is an optimal spectral window for food detection, and jamming avoidance responses and competition for sound space can hamper the bat's ability to find and track prey, a mechanism of acoustic niche partitioning may be responsible for the exceptional diversity of bat species crowding the tropical night skies. We here investigate the role of atmospheric sound attenuation in shaping the macroecological patterns of echolocating bat species richness. We hypothesize that attenuation provides more room to the coexistence of species that overlap in call frequencies by diminishing the interference between neighbor conspecific and heterospecific callers. First, we compare a set of models of environmental variables to determine what is the best combination of variables explaining the bat richness gradient. If atmospheric attenuation is a driver of species richness, we expect a combination of temperature and humidity to be the environmental variables that best explains the diversity of echolocating bats, and

also expect that this model does not offer a good prediction of Pteropodidae species richness. Second, we explicitly model the effect of atmospheric sound attenuation on a range of frequencies used by bats, correlating it to the species richness gradient in a non-linear fashion.

### 3.2 Material and Methods

We obtained geographical range maps of 1056 bat species from the IUCN global mammal assessment (IUCN 2013) to estimate the distribution of bat species richness, using a 110 x 110 km (approximately 1° at the equator) equal area grid in Mollweide projection. For each grid cell, we also extracted the average annual mean temperature (Bio01), annual precipitation (Bio12), and annual mean moisture index (Bio28), from the CliMond v1.1 dataset (Kriticos *et al.* 2012), as well as the mean annual relative humidity (ARH; New *et al.* 2002), using the package `raster` 2.3-12 (Hijmans 2014) in R 3.1.2 (R Core Team 2014).

To evaluate our hypothesis, we compared 14 candidate generalized linear models fitted on the dataset excluding Pteropodidae using both Akaike Information Criterion (AIC) and spatial leave-one-out cross-validation (SLOOCV), as proposed by Le Rest *et al.* (2013, 2014). AIC and cross-validation are asymptotically convergent for independent residuals (Stone 1977), but SLOOCV ensures model selection with the best predictive ability by taking into account spatial autocorrelation in the data. Given that Buckley *et al.* (2010) showed that Chiroptera richness presents a strong relationship with mean temperature, we used it as our most basic model, through which we derived a distance buffer of 7000 km (Figure S2) for use in the SLOOCV. The other models were composed of temperature and one of the other environmental variables (Bio12, Bio28, or ARH), and the corresponding quadratic terms for one or both variables in the model (Table 1). All predictor variables were transformed into z-scores before the analyses, and all models used a negative binomial error distribution with log link function.



After selecting the best model that explains the richness gradient of echolocating bats, we refitted it using only the grid cells with no record of Pteropodidae species (183 species, Figure 1B), and used the mean squared prediction error (MSE) to compare its predictive ability in estimating the richness patterns of non-echolocating species. In addition, we evaluated the predictive ability of the model composed just by mean temperature, and the two models with log-likelihood values closest to the best one. As most Pteropodidae species occupy tropical latitudes, we repeated the process after excluding the family Phyllostomidae (173 species) – that accounts for most of the richness in the Neotropics – from the training set of echolocating bats (Figure 1).

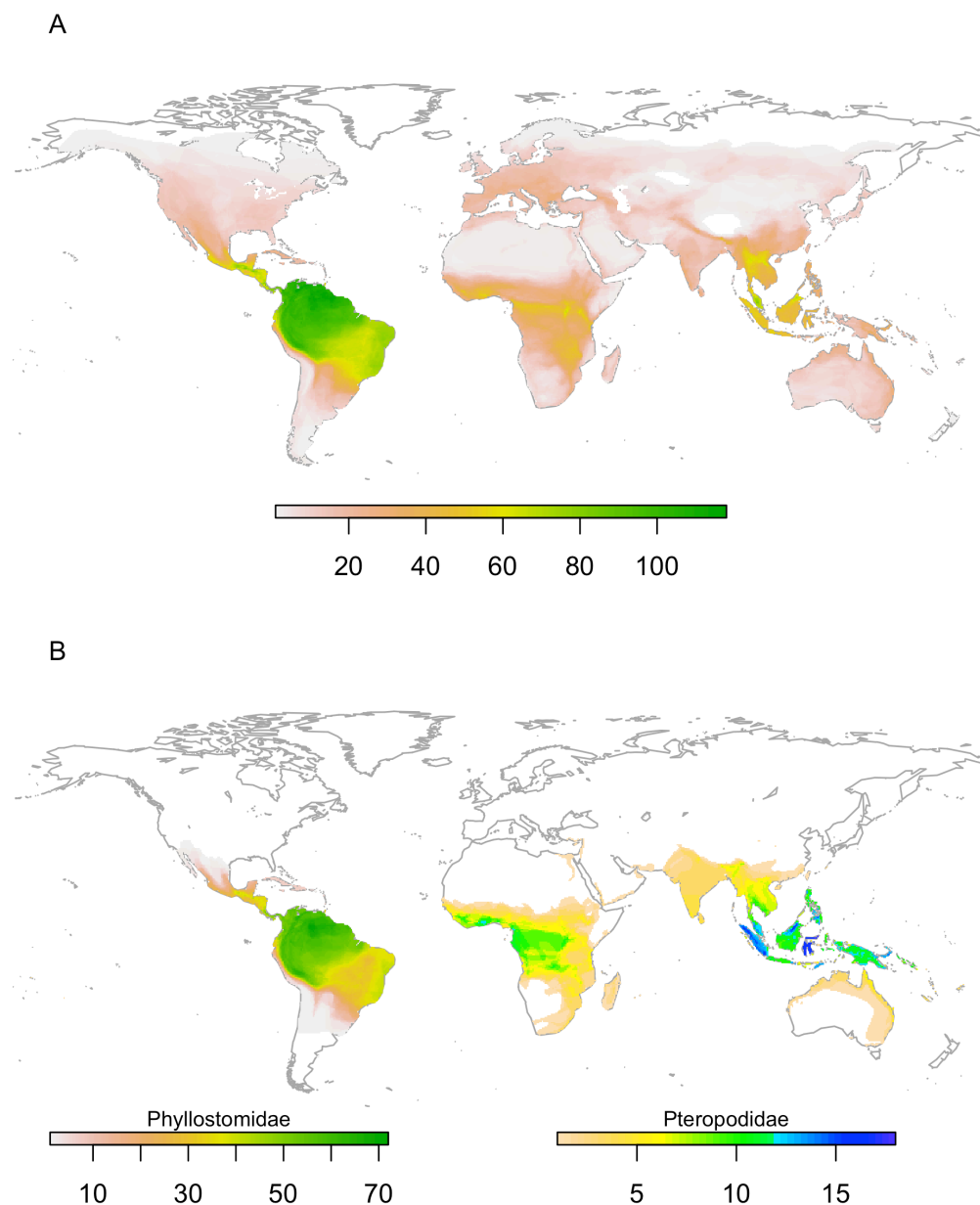


Figure 1: Species richness maps for: (A) all Chiroptera; and (B) Phyllostomidae, restricted to the New World region, and Pteropodidae, restricted to the Old World and Australasia. Note that the richness scales differ between families. The colored region in the Old World and Australasia was removed from the training set before fitting the predictive models (see text). To facilitate visualization, the maps are not projected.

To more directly investigate the relationship between sound attenuation and richness of echolocating bats, we constructed a total of 18 rasters of atmospheric sound attenuation (ASA), at a resolution of ten arcseconds, for sound frequencies between 10 and 180 kHz in 10 kHz intervals. These were constructed using the temperature and relative humidity rasters Bio01 and ARH within the formula of atmospheric sound attenuation from ISO 9613-1 (ISO 1993), assuming 1 atm pressure, and the mean values were extracted for each grid cell as above. As expected, this data show strong collinearity (Figure S3). Thus, we used variance inflation factors (VIF) to select the maximum amount of attenuation variables within the threshold VIF of 10, using the R package `usdm` 1.1-12 (Naimi 2013). This resulted in the selection of the ASA rasters of ten (ASA10), 50 (ASA50) and 180 kHz (ASA180).

These three variables were used to model echolocating bat richness within a Generalized Additive Model (GAM, Hastie & Tibshirani 1990) framework, using the R package `mgcv` 1.8-3 (Wood 2006). This method applies non-parametric smoothers to each predictor and calculates the additive component response, avoiding the necessity of assumptions about the relation between richness and ASA. However, the performance of this method can be hampered by what Wood (2006) called “concurvity”, i.e. when one parameter is itself a smooth function of another parameter in the same model. Given that this was identified between the ASA values of 50 and 180 kHz, we excluded the ASA180 term from the analyses because frequencies that high are less common than those around 50 kHz (Fenton *et al.* 1998). We also built models including the moisture index Bio28 to account for other sources of sound attenuation not captured by the ASA variables. Models combining ASA10 with the other 15 ASA variables are summarized in the supplementary Table S1 and Figure S4. A negative binomial distribution was selected, with a log link function, and a gamma value of 1.4 was used to penalize model’s excessive “wiggliness” (see Wood 2006). Explained deviance was used to summarize the model’s ability to explain the bat richness pattern, and AIC was used to select among models using different smooth functions. The contribution of each explanatory

variable was measured through the deviance reduction associated with dropping each term from the model. After selecting the best model, we refitted it including grid cells' spatial coordinates within a bivariate spherical spline, restricted to 100 degrees of freedom, to quantify the amount of deviance left unexplained by the original model and that can be explained by the spatial dependency among grid cells. We did not include this smooth term in the first place since all other variables are spatially structured, and thus subject to significant concurvity with the purely spatial term (Hawkins & Diniz-Filho 2004).

TABLE 1: Models evaluated for explaining the richness of echolocating bats.  $\Delta AIC$  was directly established from GLMs, while SLOOCV logLik was determined through spatial leave-one-out cross validation. Bold values depict the favored models pointed by each approach.

Model	$\Delta AIC$	SLOOCV logLik
~ Bio01	7905.12	-42318.32
~ Bio01 + Bio12	3055.60	-38170.48
~ Bio01 + Bio28	2339.55	<b>-38125.87</b>
~ Bio01 + RH	3100.23	-38229.04
~ Bio01 + Bio01 <sup>2</sup>	7846.71	-43677.90
~ Bio01 + Bio01 <sup>2</sup> + Bio12	2396.57	-39058.24
~ Bio01 + Bio01 <sup>2</sup> + Bio28	1834.36	-39278.71
~ Bio01 + Bio01 <sup>2</sup> + ARH	2600.56	-38886.05
~ Bio01 + Bio01 <sup>2</sup> + Bio12 + Bio12 <sup>2</sup>	805.78	*
~ Bio01 + Bio01 <sup>2</sup> + Bio28 + Bio28 <sup>2</sup>	<b>0.00</b>	-40580.58
~ Bio01 + Bio01 <sup>2</sup> + ARH + ARH <sup>2</sup>	2437.19	-39627.71
~ Bio01 + Bio12 + Bio12 <sup>2</sup>	1477.10	*
~ Bio01 + Bio28 + Bio28 <sup>2</sup>	444.81	-38902.45
~ Bio01 + ARH + ARH <sup>2</sup>	2789.84	-38892.00

\* Both models including the second order polynomial for Bio12 suffered from numerical instability in modeling the negative binomial dispersion parameter.

One important point must be emphasized: even though the relative humidity is commonly used in biological studies, it is not a direct measure of the quantity of water vapor in air, but a ratio of the actual moisture in relation to what could exist

without condensation in the same conditions of temperature and pressure (Anderson 1936), and does not have a direct biological impact over the organisms (Anderson 1936, Kurta 2014). The capacity of the atmosphere to hold water increases with temperature, and therefore the same relative humidity at different temperatures translate into very different atmospheric moistures. To account for this problem, we used a moisture index (Kriticos et al. 2012) that is independent of temperature (Hutchinson *et al.* 2009). For consistency with the formula of atmospheric sound attenuation (ISO 1993), we also evaluated models using a global measure of relative humidity (New *et al.* 2002), but we expect the moisture index to be a better explanatory variable in the linear models. Moreover, the moisture index accounts for condensed water in the environment, what alters the reflectance of incident sound waves by diminishing porosity (Kuttruff 1991, Attenborough 2007).

### 3.3 Results

Mean annual moisture index was selected through SLOOCV as the best environmental variable, in combination with temperature, to explain the richness gradient of echolocating bats. Model selection using AIC supported the model including second order polynomials for both Bio01 and Bio28 as the best one (Table 1), with all other models completely disfavored by their respective Akaike weights. On the other hand, SLOOCV supported the simpler model composed only by Bio01 and Bio28 as the best fit, and models adding the annual precipitation and ARH appeared as second and third best models, respectively. SLOOCV evaluates models by means of their predictive ability, so these were used to predict the richness patterns of Pteropodidae.

Prediction of the richness of non-echolocating bats by the selected model was worse than predictions based on two of the three other models evaluated (Table 02). Although the model composed only by mean temperature presents the lowest MSE, its better performance can be accounted for by the smaller range of predicted

values, closer to the maximum range of observed Pteropodidae richness values (Figure 02). As can be seen in the density curves, the temperature model predicted most of the richness above 20 species, a value not even encountered in any grid cell. All these models greatly overestimate the richness of non-echolocating bats, with mean values between 32 and 64 species. The same patterns hold after excluding Phyllostomidae (results not shown).

Table 2: Mean squared errors (MSE) of predictions associated with each model. Pteropodidae MSE refers to predicting this family richness based on the model adjusted to echolocating species, while Echolocating bats MSE was calculated through ten-fold cross validation.

<b>Model</b>	<b>Pteropodidae MSE</b>	<b>Echolocating bats MSE</b>
Bio01 + Bio28	2979.24	396.88
Bio01 + Bio12	24805.23	2292.62
Bio01 + ARH	1226.08	280.66
Bio01	842.44	525.80

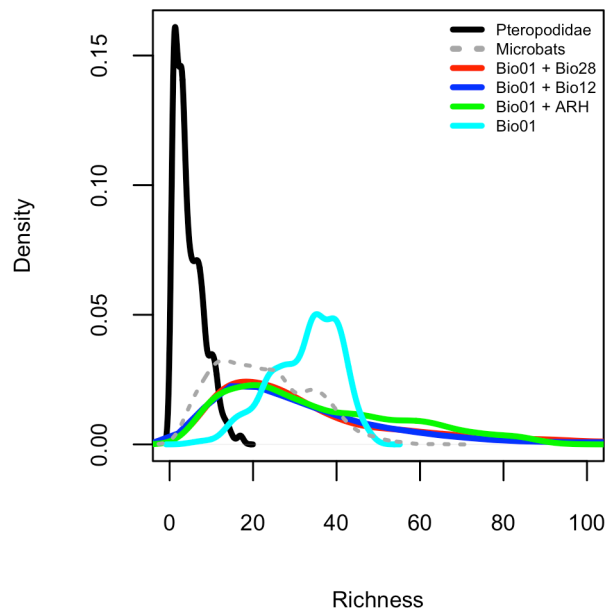


Figure 02: Density plot of the observed Pteropodidae richness gradient, and four model predictions (see text). Grey dashed line (microbats) represents the density of echolocating species in the cells with Pteropodidae species. Abscissa is truncated at 100 species, but the first two models extend beyond it.

A GAM model composed with separate smoothing parameters for each attenuation variable (ASA10, ASA50), and including Bio28, provides the best balance of explanatory power without excessive wiggleness. This model accounts for 79.2% of the deviance in the richness gradient, with a total of 58.79 estimated degrees of freedom. The shape of the response curves varied among variables (Figure 03). The model without Bio28 has a significant drop in explained deviance, accounting for 70.9% of the variance. For comparison, a GAM composed by Bio01 and ARH explains 67.6% of the deviance. ASA50 was the most important variable explaining deviance in the richness gradient, followed by Bio28 (Table 03). The model including a smooth function of spatial coordinates explains significantly more deviance in bats' richness, 96.7%. Its concurvity, however, is almost one with all other smoothing parameters. Allowing more degrees of freedom to the spatial function results in even higher explained deviances, as more localized smooth curves are created, and lead to less wiggle smooth curves to the other model terms, but with increased concurvity (Supplementary figures S5 to S8). The results shown by the other ASA variables follow the same pattern of the selected model (Table S1 and Figure S4).

Table 03: Estimated degrees of freedom, percentage explained deviance, residual deviance and drop contribution for the smooth terms included in the GAM for echolocating bat richness. The first model is the selected one that better explains the richness patterns. Contribution of each term is represented by the difference in residual deviances between the favored model and the model without the respective variable. The fifth model represents the favored model plus a spatial smooth spline.

<b>Model</b>	<b>EDF</b>	<b>Explained deviance (%)</b>	<b>Residual deviance</b>	<b>Deviance difference</b>
ASA10 + ASA50 + Bio28	58.79	79.2	8511.5	
ASA50 + Bio28	42.75	74.7	8692.9	- 181.38
ASA10 + Bio28	48.05	65.4	9205.4	- 693.92
ASA10 + ASA50	34.71	70.9	8984.4	- 472.96
ASA10 + ASA50 + Bio28 + LatLong	138.54	96.7	7391.3	1120.2
Bio01 + ARH	33.51	67.6	9176.7	-665.22

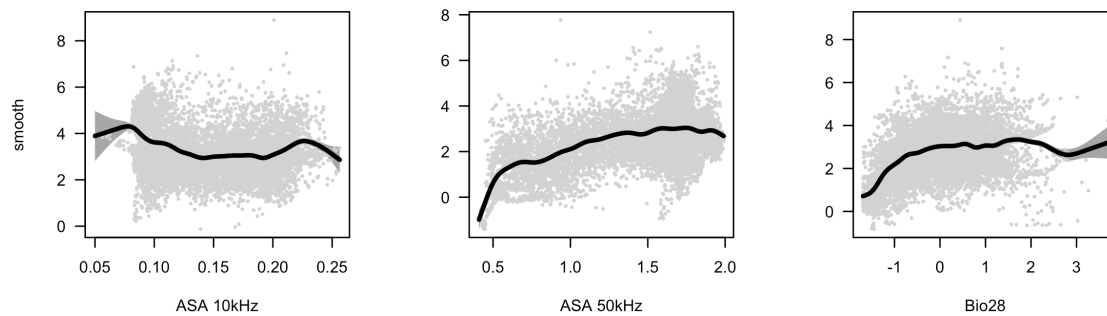


Figure 03: Response functions for the echolocating bat richness on the three environmental variables included in the GAM. The shaded areas around the smooth curves represent 95% confidence intervals, but note that it is very narrow for the major part of the curves. Points are the respective partial residuals when holding the other covariates at their median values.

### 3.4 Discussion

Our main goal was to evaluate the hypothesis that sound attenuation is important in determining the richness of echolocating bats, offering a mechanism through which local scale interactions mediated by the environment can integrate to structure coarse scale patterns. That prediction is supported by the finding that temperature and moisture are the best set of predictors of bat richness. If this relationship was purely mechanistic on these variables, or a matter of evolutionary processes alone (Tello & Stevens 2010, 2012), we should find this model to be a good predictor of Pteropodidae species richness. Our findings, however, point to a great overestimation of this family's richness, and the simpler model composed just by mean annual temperature as a better predictor. Models that analyze all bat species as a whole do not recognize this difference, and suggest temperature alone as the best predictor of bat richness (Buckley *et al.* 2010).



Body size may be responsible for the richness difference between Pteropodidae and other species inhabiting this region, as larger species are expected to have larger ranges (Meiri & Thomas 2007). Species richness is not correlated with body size in Chiroptera (Isaac *et al.* 2005), and whether or not Pteropodidae are significantly larger than other bats, based on its phylogenetic relationship with other groups, still waits investigation (but see Hutcheon & Garland 2004). Nevertheless, we did not find a significant difference between ranges of Pteropodidae and species of other families ( $F = 62.63$ ,  $p = 0.53$ ; see Supplementary material and methods), nor a relationship between body size and range area within Pteropodidae ( $F_{1,154} = 0.35$ ,  $p = 0.56$ , Figure S9). At least in New World bats, there is no sign of an clade age-area relationship (Weber *et al.* 2014) nor phylogenetic signal determining range areas (Villalobos *et al.* 2013), and thus other mechanisms such as geographical constraints (Jetz & Rahbek 2002) or biotic interactions (Wiszniewski *et al.* 2013) must be responsible for delimiting species ranges.

Although atmospheric sound attenuation is expressed by a non-linear function of temperature and relative humidity, we found the moisture index to be a better explanatory variable for the richness gradient in the linear models. Contrary to relative humidity, this variable is independent from temperature, and accounts not only for air humidity, but also for general humidity condensed in soil and vegetation (Hutchinson *et al.* 2009). That can contribute to attenuation of echolocation pulses reaching these surfaces (Yang *et al.* 2013), and alter the capabilities of bats in discerning prey close to the background (Schmieder *et al.* 2012). In the evaluated generalized additive models, the moisture index explains a significant proportion of the deviance, depicting a general trend of higher richness with increasing moisture.

Explicitly modeling sound attenuation reveals a slightly complex relationship between low frequency attenuation, namely at 10 kHz, and richness. The GAM smooth curve shows that higher species richness is encountered at both lower and higher attenuation coefficients at this frequency. We note, however, that experimental evidence must be gathered to determine if the absolute values of attenuation at this frequency have biological relevance. Attenuation at 50 kHz, on

the other hand, favors our hypothesis that higher richness is coupled with higher atmospheric sound attenuation. The variation in attenuation at this frequency is proportional to that at 10 kHz, but the biological impact is probably much higher. Disregarding other sources of sound attenuation, a bat calling at 120 dB and 50 kHz, and with a hearing threshold of 20 dB (Surlykke & Kalko 2008), spread its call for 100 m at the lower end of the attenuation gradient, but only 25 m at the more attenuating environments. This smaller range affects not just the emitter of the call, but also allows smaller inter-individual spacing. Moreover, the frequency of 50 kHz was analyzed because it represents the phylogenetic mean value for bats (Bilski *et al.* – Chapter 2), and is in the frequency window best suited for insect detection (Fenton *et al.* 1998), but several species are known to emit frequencies much higher (e.g. Holderied & von Helversen 2003, Schmieder *et al.* 2012), and thus are subject to much higher ASA.

Vegetation is also known to contribute to sound attenuation at high frequencies, both through sound wave absorption and scattering (Bullen & Fricke 1982, Yang *et al.* 2013). Adding NDVI (extracted from FAO 2008) to the selected GAM, however, adds just a minor contribution to the explained deviance, increasing it from 79.2% to 79.9% (not shown). Also, there is a high concurrency between Bio28 and NDVI, but exchanging Bio28 for NDVI diminishes by 1% the explained deviance. Vegetation probably exerts an attenuation effect more complex than what can be captured by NDVI alone, but modeling forest sound attenuation is not trivial (Fricke 1984), even more at the macroecological scale.

Bats are known to adjust echolocation time-frequency structure (Guillén *et al.* 2000, Murray *et al.* 2001, Fenton *et al.* 2011) and call intensity (Surlykke & Kalko 2008, Brinklov *et al.* 2010) to effectively probe the environment. Despite that, interspecific variation in the frequency-time domain appears to be more constrained by phylogenetic history than spatial effects (Bilski *et al.* - Chapter 1), so that closely related species have more similar echolocation call structures. In this scenario, environments with pronounced ASA provide more room to the maintenance of closely related species with minor differences in call structure, given that competition for the sound space is reduced.

Herein we provide an ecological hypothesis that can mechanistically link a process of local scale niche partitioning to the coarse scale macroecological association between species richness and environmental variables. At the large scale, attenuation can act as a condition (*sensu* Soberón 2007) for the species persistence in suitable areas, while at the community scale it shall act through alleviating the competition for the acoustic niche and allowing the coexistence of bat species in similar functional guilds. The macroecological pattern described in this matter must be put to test at community scale studies that thoroughly characterize the echolocation calls of all component species, as well as their activity patterns, to confirm if greater sound attenuation allows the coexistence of species with similar call frequencies.

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### 3.6 Supplementary material

Figure S1: Atmospheric sound attenuation in relation to relative humidity, in air temperatures of 0°C, 5°C, 10°C, 15°C, 20°C, 25°C, 30°C and 35°C at sea level. From bottom to top, each curve represents a sound frequency between 10 and 180 kHz, in 10 kHz intervals. Dotted lines are the selected reference frequencies of 10, 50 and 180 kHz (see main text).

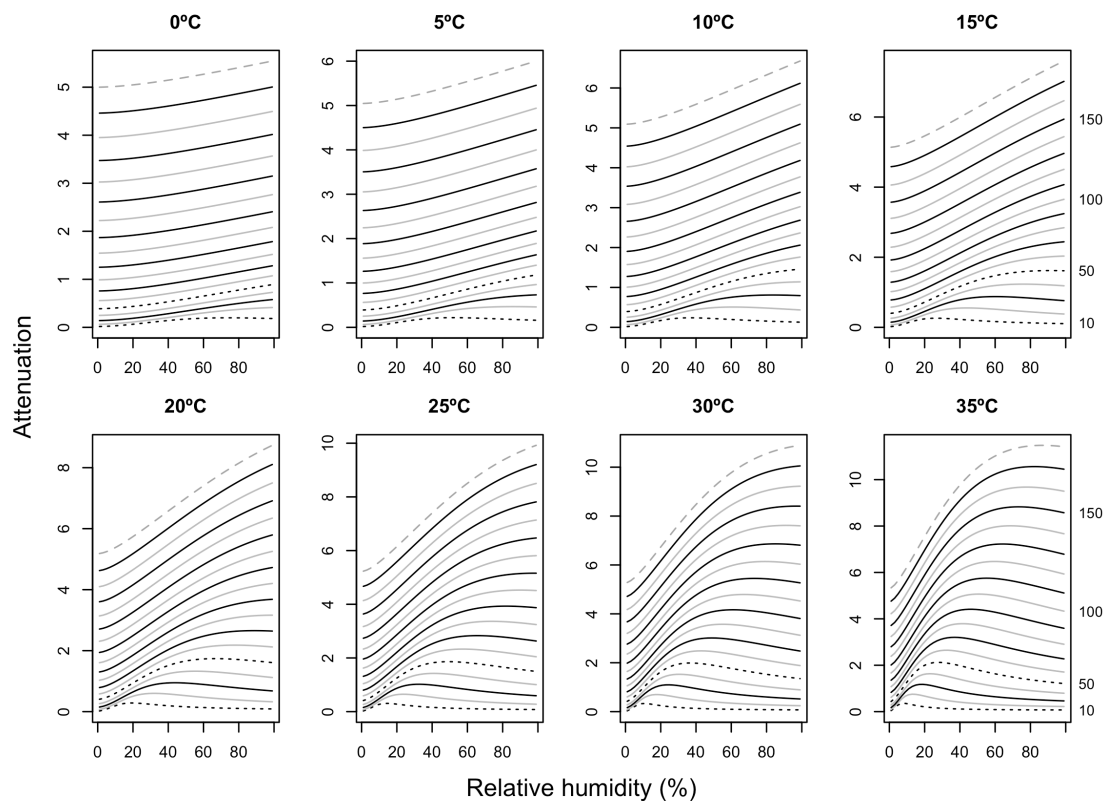


Figure S2: Semivariogram of the deviance residuals from the model between species richness and mean annual temperature.

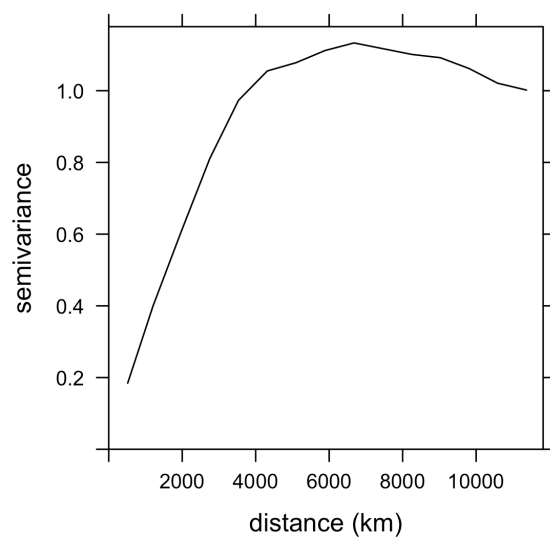


Figure S3: Correlation plot of the atmospheric sound attenuation variables.

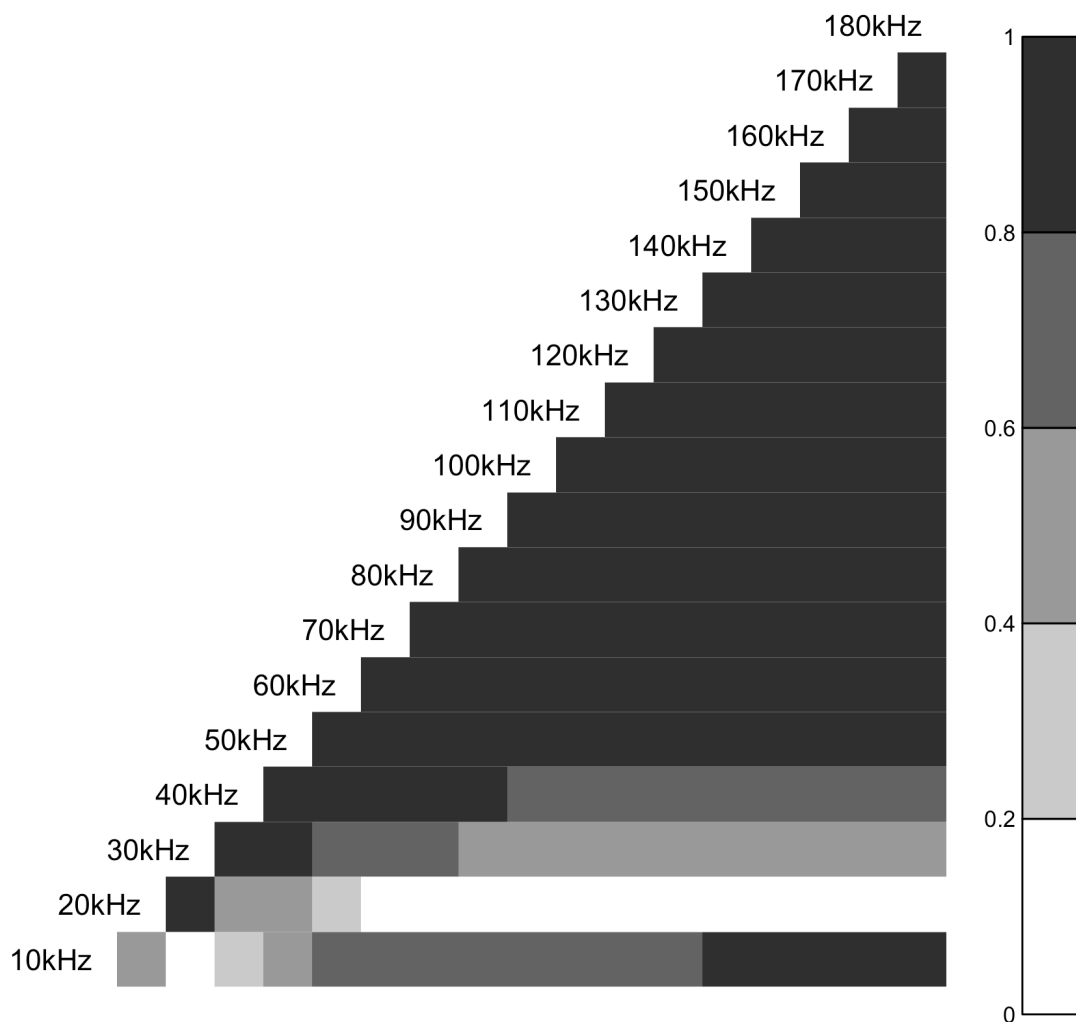


Figure S4: Response functions of the echolocating bat richness. The first and third variables, ASA10 and Bio28, are held constant among models, while the second plot depicts ASA variables between 20 and 180 kHz. The plot for ASA50 is depicted in the text.

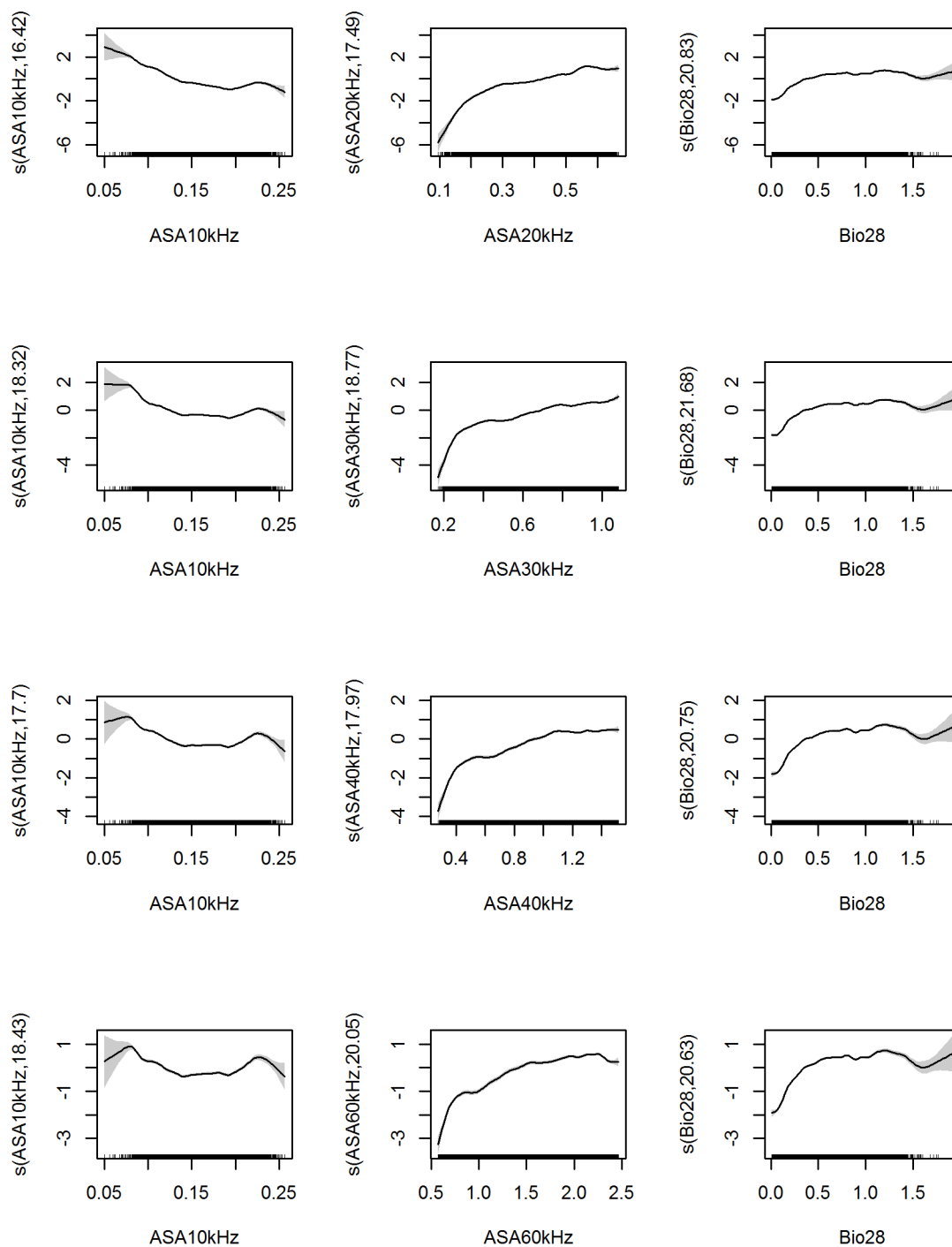


Figure S4 (continued):

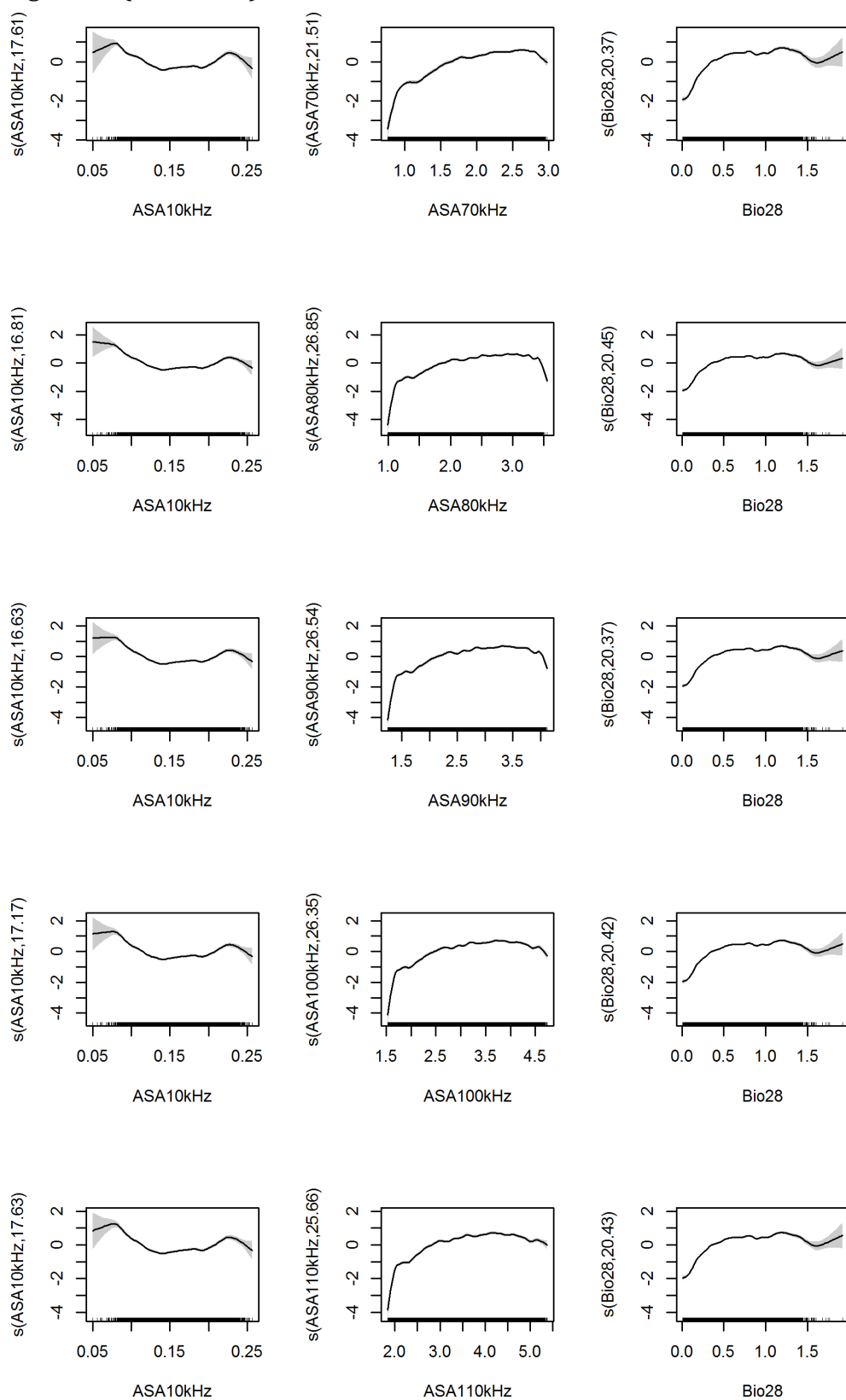


Figure S4 (continued):

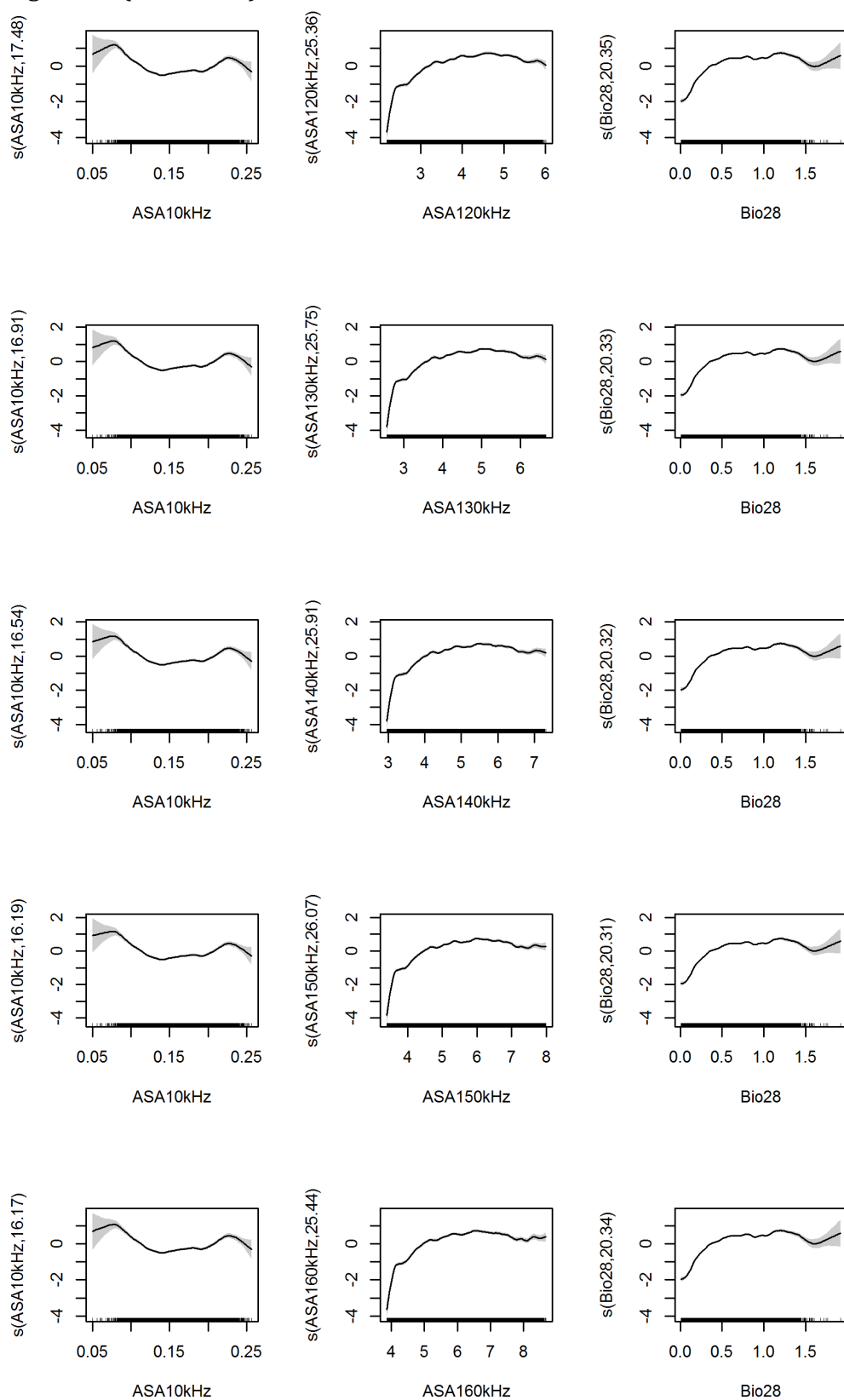


Figure S4 (continued):

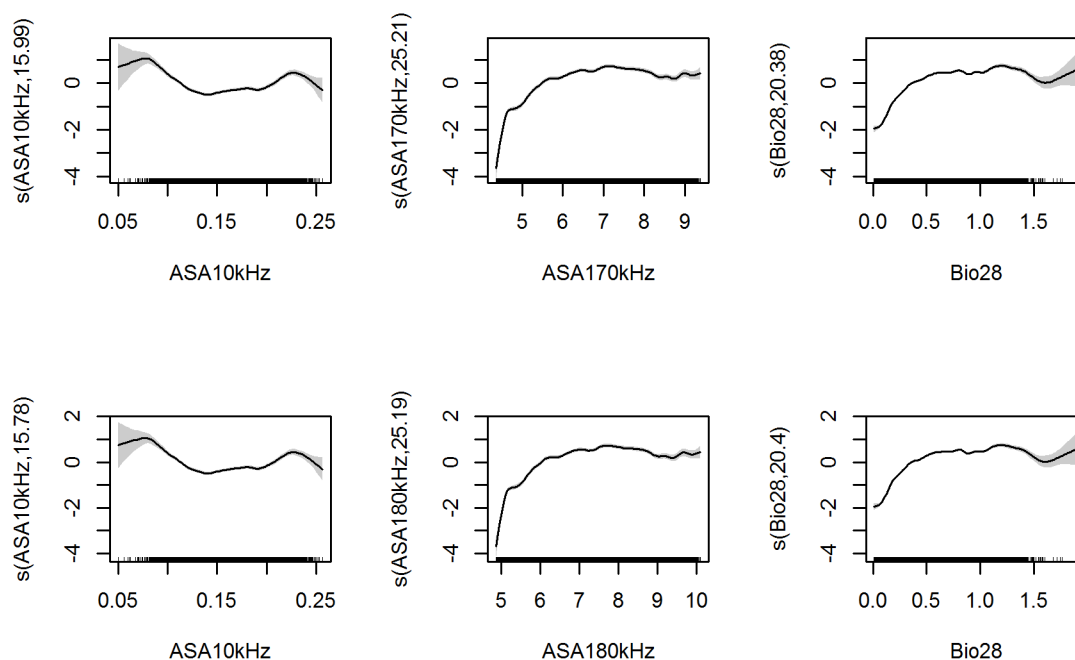


Table S1: Estimated degrees of freedom, percentage explained deviance and residual deviance for all evaluated Generalized Additive Models.

Model	EDF	Explained deviance (%)	Residual deviance
ASA 10 + ASA 20 + Bio28	78.77	55.74	8557.41
ASA 10 + ASA 30 + Bio28	78.79	59.76	8541.93
ASA 10 + ASA 40 + Bio28	78.97	57.41	8531.93
ASA 10 + ASA 50 + Bio28	79.19	58.79	8511.48
ASA 10 + ASA 60 + Bio28	79.47	60.11	8500.45
ASA 10 + ASA 70 + Bio28	79.60	60.49	8484.62
ASA 10 + ASA 80 + Bio28	79.89	65.11	8466.13
ASA 10 + ASA 90 + Bio28	79.82	64.54	8466.16
ASA 10 + ASA 100 + Bio28	79.75	64.93	8475.28
ASA 10 + ASA 110 + Bio28	79.70	64.72	8482.72
ASA 10 + ASA 120 + Bio28	79.68	64.19	8485.47
ASA 10 + ASA 130 + Bio28	79.69	63.99	8481.76
ASA 10 + ASA 140 + Bio28	79.71	63.78	8480.01
ASA 10 + ASA 150 + Bio28	79.74	63.57	8477.72
ASA 10 + ASA 160 + Bio28	79.73	62.94	8480.72
ASA 10 + ASA 170 + Bio28	79.73	62.58	8479.16
ASA 10 + ASA 180 + Bio28	79.75	62.37	8475.94

Figure S5: Response functions of the echolocating bat richness including a bivariate spatial smooth. The three upper plots represent the curves of the three investigated variables (see text). Lower plots depict four views of the spatial smooth, restricted to 100 degrees of freedom.

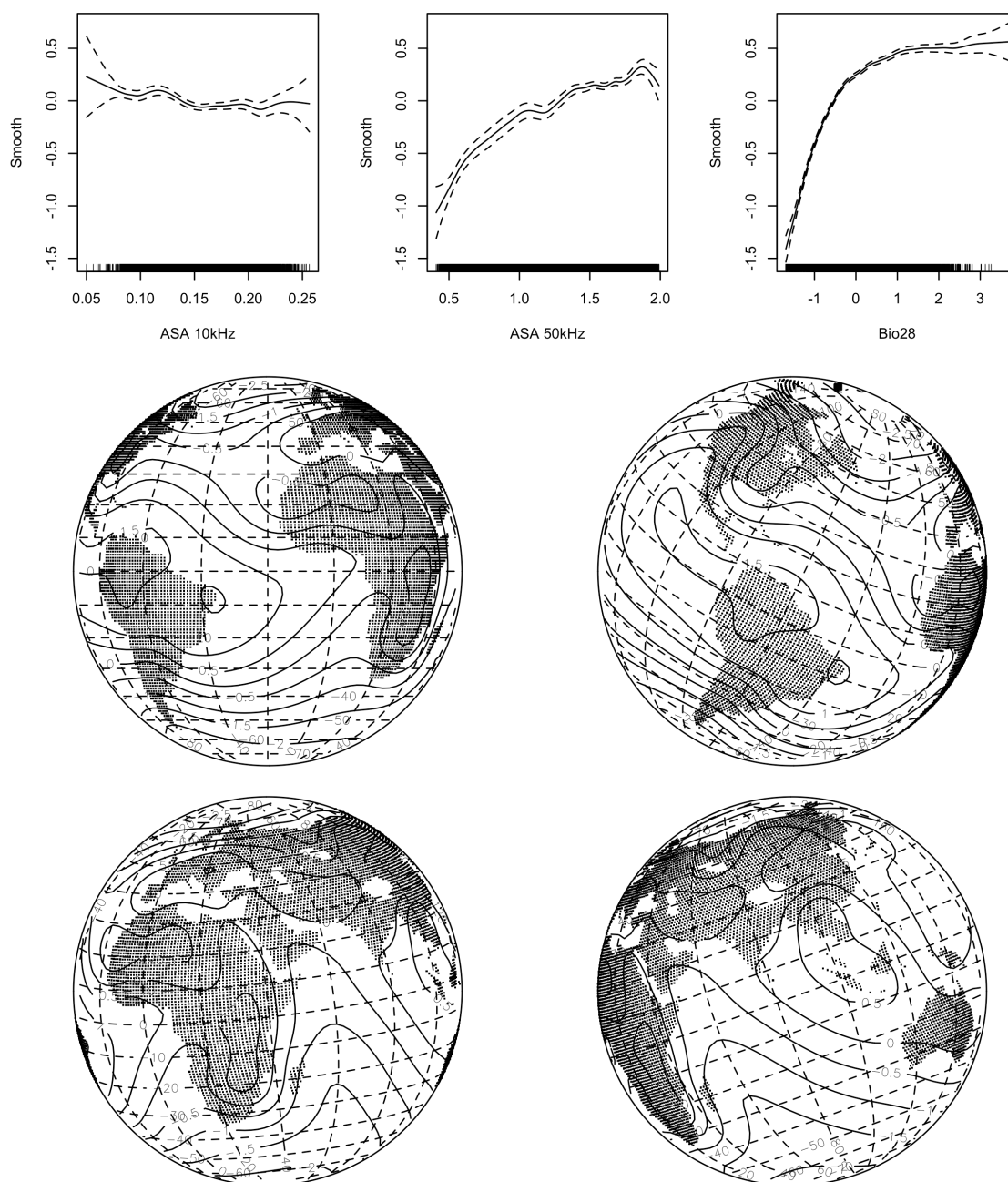




Figure S6: The same as figure S5, but allowing 200 degrees of freedom to the spatial smooth term. Note the increase in spatially restricted curves.

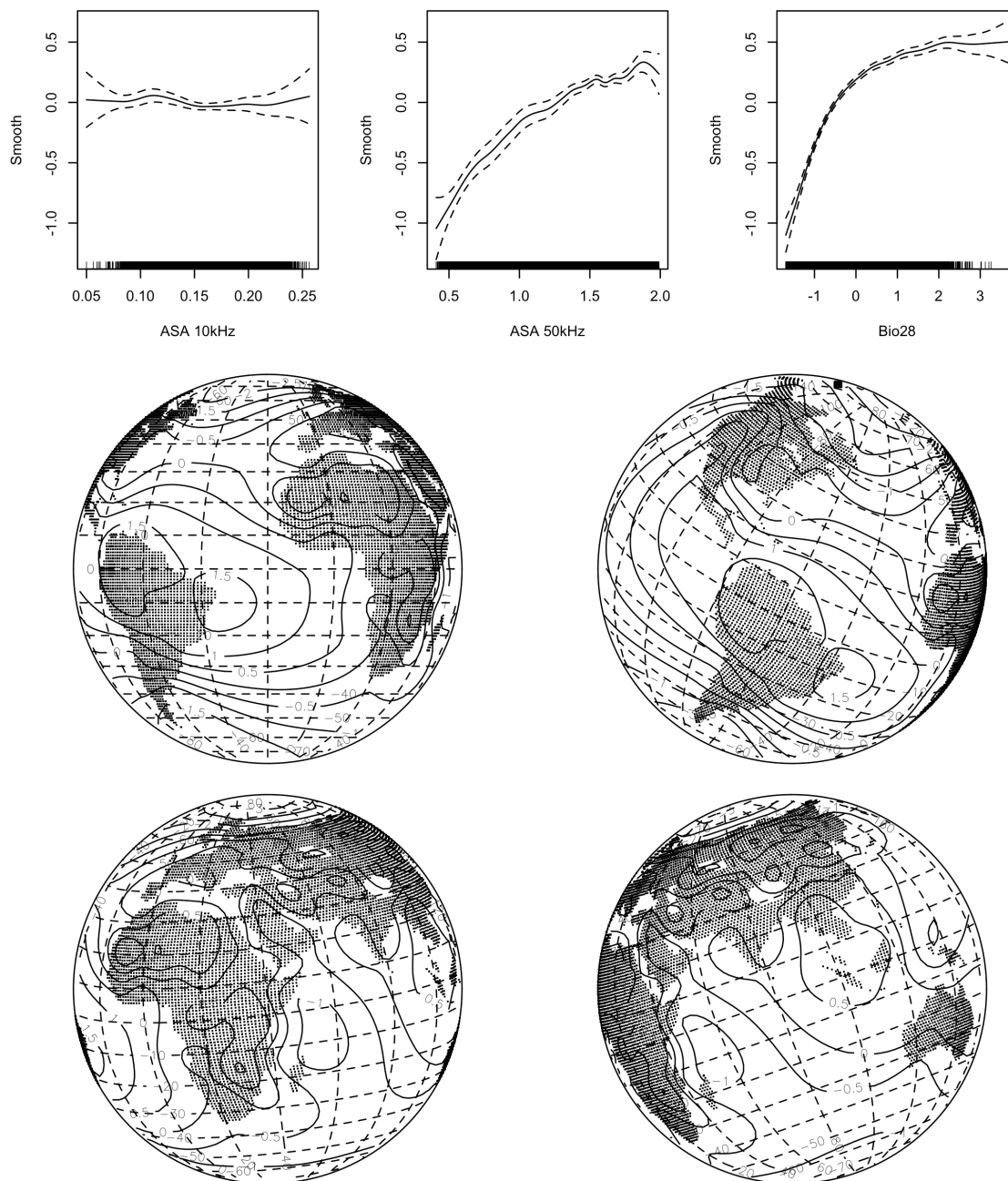


Figure S7: The same as figure S5, but allowing 300 degrees of freedom to the spatial smooth term. Note the increase in spatially restricted curves.

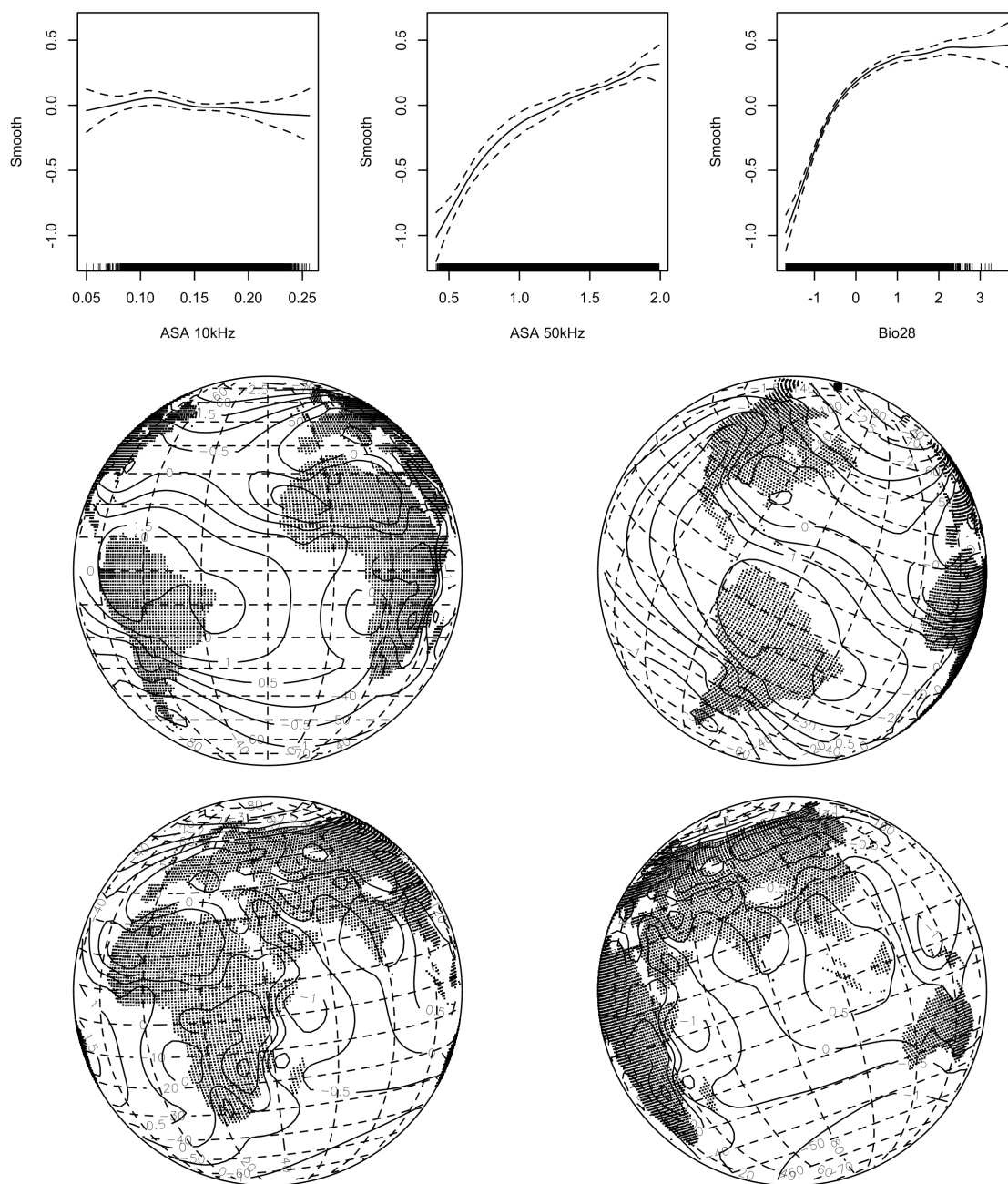
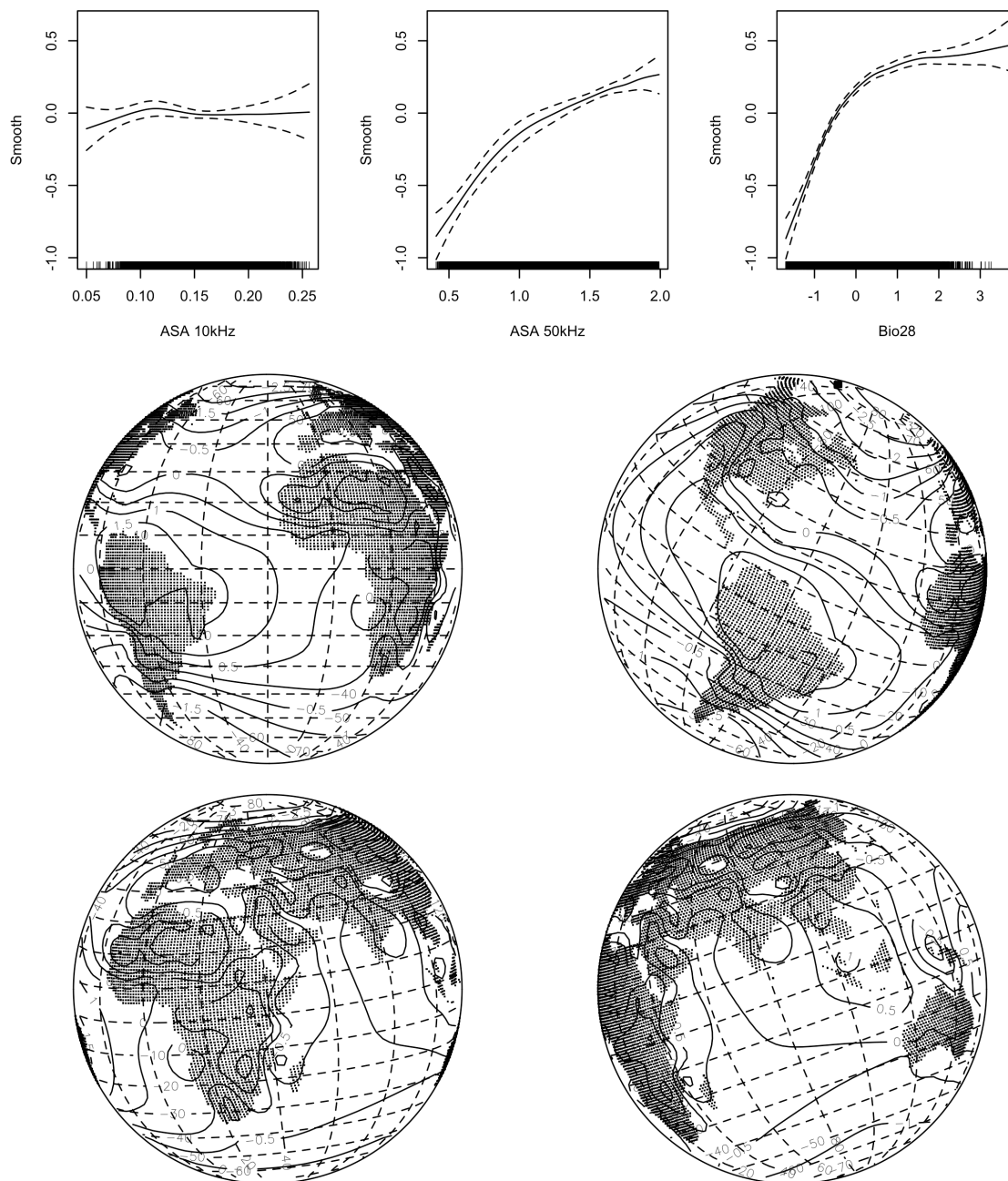


Figure S8: The same as figure S5, but allowing 400 degrees of freedom to the spatial smooth term. Note the increase in spatially restricted curves.

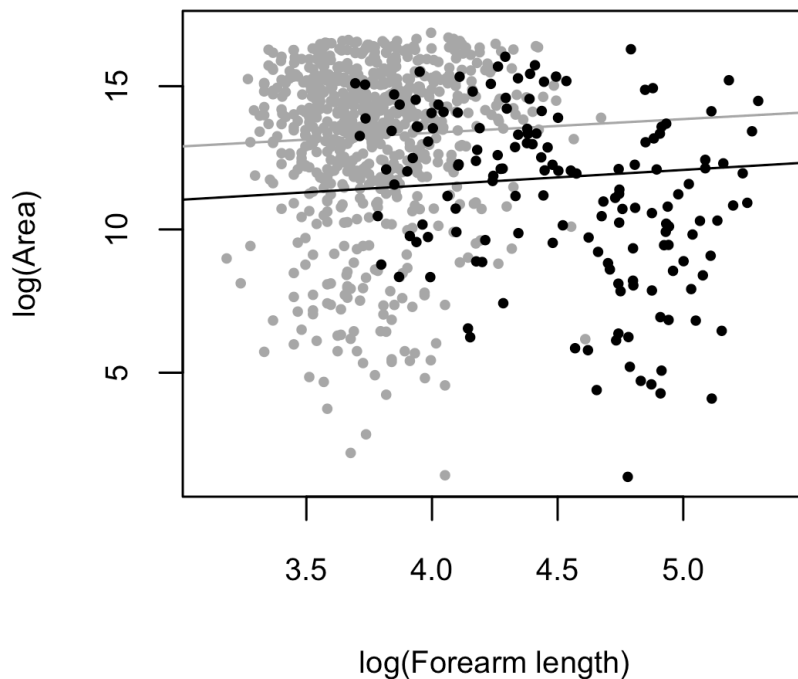


## Supplementary Material and Methods

To evaluate if there is a difference between the distribution areas of Pteropodidae and echolocating species, we extracted the range areas based in the same distribution polygons (see main text), using the R package `rgeos` 0.3.8 (Bivand & Rundel 2014). To correct for the phylogenetic non-independence in the data, we used the phylogenetic tree of Fritz *et al.* (2009), and compared the mean ranges between Pteropodidae and echolocating species using the phylogenetically corrected ANOVA (Garland *et al.* 1993) function `phylANOVA` in the package `phytools` 0.4-31 (Revell 2012).

To examine the correlation between range areas and body size in the family Pteropodidae, we extracted data on the species' forearm length from the PanTHERIA database (Jones *et al.* 2009). We applied a generalized least squares regression with a phylogenetic correlation structure (`corPagel` from the package `ape` 3.1.4), to account for the phylogenetic relation among species. In all analyzes we used log transformed variables.

Figure S9: Regression of distribution range area on forearm length for 854 species. Grey dots represent 698 species of echolocating bats, while the black dots are 156 species of Pteropodidae. Regression line coefficients are:  $\beta = 0.48$ ,  $t = 0.98$ ,  $p = 0.32$  and  $\beta = 0.52$ ,  $t = 0.59$ ,  $p = 0.55$ , respectively.



### Supplementary references:

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